SPTREMBL_19:* Database :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp_invertebrate:*
sp_mammal:*
sp_mhc:* sp_vertebrate:*
sp_unclassified:* sp_rvirus:*
sp_bacteriap:* sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:* sp_organelle:* sp_archeap:* sp_plant:* sp_rodent:* sp_virus:* sp_phage: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			Description		233231 SLIEPLUCUCC	Volgic peptostrept	OE303	Casala streptococc	Colibb arabidopsis	Q93em8 streptococc	Q9skp0 arabidopsis	096246 arabidonsis	003+116 otanhii oco	OOJOET TOCOC	Oction Petromyzon	U954KZ IACTODACILI	Q9wza6 thermotoga	Q9u459 plasmodium	053837 galmonella	Odubar manduce	אינייייייייייייייייייייייייייייייייייי	. Osjyka neisseria m
COMMAKIES			ID	053291	051912	051918	053975	0.000	COSEMB	OFFICE	CSSKPO	096246	093TY6	091255	095482	7 4 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	COWCAO	090459	053837	0908G8	OG TVKA	******
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ALIGNMENTS

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Pfam; PF02246; B1; 4.
Pfam; PF01468; GA; 4.
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395 KPEE 398
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Matches 246;
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AYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTA 180
         EFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKA 240
                                              241 NLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKVD 300
                                                                                    YRYADALKKDNGEYTVDVAÐKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAE 181
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                                                                                                                                                                                                                                                                                                                 Kastern W., Holst E., Nielsen E., Sjobring U., Bjorck L.;
"Protein L, a bacterial immunoglobulin-binding protein and possible
virulence determinant.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptostreptococcus magnus.
Bacteria: Firmicutes; Bacillus/Clostridium group; Clostriddaceae;
                                                                                                                                                                                                                                                                                                                                                                                           Bjoerck L., Sjoebring U., Kastern W.;
"Structure of peptostreptococcal protein L and identification of repeated immunoglobulin light chain-binding domain.";
J. Biol. Chem. 267:12825(1992).
EMBL; M86697; AAA25612.1;
InterPro. IPR001847; B1.
InterPro: IPR001899; Gram_pos_anchor.
Pfam; PF00246; B1: 5.
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719 PROTEIN L.
78983 MW; 963A8D76D5E34DD2 CRC64;
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Last annotation update)
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Similarity 100.0%; Pred. No. 2.5e-78;
04; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92316971; PubMed=1618782;
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719 AA;
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EKPEE 326
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Matches 304;
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"Nucleotide sequence of the gene for peptostreptococcal protein L.";
DNA Seq. 4:259-265(1994).
EMBL: L04466; AAA67503.1; -.
HSSP: Q51911; 1GAB.
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Bacteria: Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
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25 992 PROTEIN L.
992 AA; 108700 MW; 9CFF5771578A5DCE CRC64;
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Last annotation update)
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Interpro, IPR002988; GA.
Interpro, IPR001899; Gram_pos_anchor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=3316;
MEDLINE=95078460; PubMed=7987012;
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P71401 haemophilus O13099 xenopus lac Q9y503 homo sapien Q9u459 plasmodium

P71401 013099 013099 09Y503 09U459 09S12 09S303 09YE5 097T80 097T80 0966489

Q9ns12 homo sapien Q95303 homo sapien Q97ye5 homo sapien Q97ye6 homo sapien Q97k80 streptococc Q9a0k5 streptococc Q9307 carasius a 069188 streptococc Q30874 streptococc Q94k48 streptococc Q94k48 streptococc Q94k48 streptococc Q91019 plasmodium Q9mi0 clostridium Q91255 petromycon Q01255 petromycon Q91255 petromycon

> 069188 033742 030874 09KK48 09ND19 093M90 091255

2692 5458 2725 2725 2725 20456 11665 11665 701 969 1368 1110 1368 11110

13 2 16

Q9JYK4 Q9Y1P8 Q9LC00 Q56193 Q56192 Q9RQT5 Q9Z4N7

> 845 1698 492 573 701

ALIGNMENTS

Q17464 Q9EY85

1873 897 3147 717

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                                                                                                                                           1 AVENKEETPETPETDSEEEV......GVDGVWTYDDATKTFTVTEM
          GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                   562222 seqs, 172994929 residues
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Maximum Match 100%
Listing first 45 summaries
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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Maximum DB seq length: 2000000000
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2235
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ö GEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAE 120 Gaps 1 AVENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDN 60 Streptococcus sp.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae; SEQUENCE FROM N.A.
MEDLINE-93094283; PubMed=1460053;
Kihlberg B.M., Sjobring U., Kastern W., Bjorck L.;
"Protein LG: a hybrid molecule with unique immunoglobulin binding properties." ; 0 Length 455; Indels 49926 MW; 381FC235BBC8307B CRC64; Created)
Last sequence update)
Last annotation update) 100.0%; Score 2235; DB 2; 100.0%; Pred. No. 1e-100; ive 0; Mismatches 0; 455 AA properties."; J. Biol. Chem. 267:25583-25588(1992). EMBL; S50809; AAA03280.1; HSSP; P06654; IPGX. InterPro; IPR00147; B1. InterPro; IPR000724; IgG_bind_B. Pfam; PF02246; B1; 4. Pfam; PF01378; IgG_binding_B; 2. PRT; Query Match 100.0%; Some Best Local Similarity 100.0%; P. Matches 434; Conservative 0; 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19, PROTEIN LG (FRAGMENT). PRELIMINARY; 455 AA; NCBI_TaxID=1306; 455 SEQUENCE NON_TER q QQ δ δ

> Q54181 streptococc Q56212 streptococc Q53974 streptococc Q5337 streptococc Q940898 manduca sex Q91f88 arabidopsis

051918 peptostrept 053975 streptococc 093em8 streptococc

Q51912 Q51918 Q53975 Q93EM8 Q54181

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1587.5 1263.5 706.5 697.5 670

126459786

DB

Length

Query

Score

Result No. 253291 streptococc 251912 peptostrept

Description

SUMMARIES

Q9skp0 arabidopsis Q9s4k2 lactobacill Q93ty6 staphylococ Q96246 arabidopsis

O9aer7 staphylococ

Q9LF88 Q9AER7 Q9SKP0 Q9S4K2 Q93TY6 Q96246

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294 182.5 182 177.5 177.5 170.5

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RPEEPMD-TYK--LILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVD-GEWTYDDATK 357
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"Nucleotide sequence of the gene for peptostreptococcal protein L.";
DNA Seq. 4.259-265(1994).
EMBL: L04466; AA67503.1; -.
HSSP: Q51911; 1GAB.
InterPro: IPR003147; B1.
InterPro: IPR0031899; Gram_pos_anchor.
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215 YRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAE
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108700 MW; 9CFF5771578A5DCE CRC64;
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Pfam; PF01468; GA; 4.
Pfam; PF00746; Gram_pos_anchor; 1.
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992 AA;
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protein and possible
                   121 AYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTOTA
                                          EFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKA
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Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
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"Structure of peptostreptococcal protein L and identification of repeated immunoglobulin light chain-binding domain.";
J. Biol. Chem. 267:12820-12825(1992).
BMBL, M86697; AAAAS512.1;
InterPro: IPR0013147; B1.
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Last annotation update)
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Kastern W., Holst E., Nielsen E., Sjobring U.,
"Protein L, a bacterial immunoglobulin-binding
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76.3%; Pred. No. 3e-69;
iive 13; Mismatches
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Pfam; PF00746; Gram_pos_anchor; 1.
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719 PRC
78983 MW;
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01-NOV-1996 (TrEMBLrel. 01,
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Matches 334; Conservative
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6 x 5 AA REPEATS OF [DEVP]-[DE]-[AT]-K-K.
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
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cus dysgalactiae.
Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                  IMMUNOGLOBIN G BINDING PROTEIN MIG.
ALPHA 2-MACROGLOBULIN-BINDING
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                                                                                            (POTENTIAL).

EXTRACELLULAR (BY SIMILARITY).

MEMBRANE ANCHOR (BY SIMILARITY).

2 X 24 AA REPEATS.

1-1.

5 X 70 AA TANDEM REPEATS

(IGG CONSTANT REGION-BINDING).
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4A41CEEF7977862A CRC64;
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POTENTIAL
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Pfam; PF01378; IgG_binding_B; 3. SEQUENCE 185 AA; 20118 MW; 1
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Goward C.R., Murphy J.P., Atkinson T., Barstow D.A.;
"Expression and purification of a truncated recombinant streptococcal
                                                                                                                                                                                                                                                                                                                                                                      203 QAVQLEAPTVIDAPELTPALTTYKLVVKGNTF--SGETTTK----AIDTATAEKEFKQYA 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          422
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                                                                                                                                                                                                                                                                                                                                             24 ANLIFANGSTQTAEFKGTFEKATSEAYAYADTLK-KDNGEYTVDVADKGYTL--NIKFA- 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus sp. 'group G'.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                 MEDLINE=21437603; PubMed=11553540;
Song X.M., Perez-Casal J., Bolton A., Potter A.A.;
"Surface-Expressed Mig Protein Protects Streptococcus dysgalactiae
against Phagocytosis by Bovine Neutrophils.";
Infect. Immun. 69:6030-6037(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                  -----GKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA--YRYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 DALKKDNGEYTVDVADKGYTLNIKFA - - - GKEKTPEEPKEEVTIKANLIYADGKTQTAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 KGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFA---GKEKTPEEPKEEVTIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314 DAATAEKEFKQYATAN---NVDGEWSYDYATKTFTYTEKPAVIDAPELTPALTTYKLIVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 ANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 DEKPE--EPMDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATK
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                                                                                                                                                                                                                                                             Length 669;
                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                      39 POTENTIAL.
669 MIG.
72682 MW; 5C8982B952029B03 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                      Query Match 31.2%; Score 697.5; DB 2; Best Local Similarity 43.5%; Pred. No. 2.3e-26; Matches 190; Conservative 49; Mismatches 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein G.",
Blochem. J. 267:171-177(1990).
EMBL; X53324; CAA37410.1; -.
HSSP; P06654; 1PGX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      543 GVWTYDDATKTFTVTEM 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               418 GVWTYDDATKTFTVTEM 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                              669 AA;
  STRAIN-ATCC 43078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                   115 EEATA---EAYRYADALK---KDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169 NLIYADGKTQTAEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKT 228
                                                                                                                                                                                                                                          305 -----EPMDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATKT 358
                                                                                                                                                                                                                                                                                                                                       FIVIEKPEVIDASELIPAVITYKLVINGKTLKGETITKAVDAETAEKAFKQYANDNGVDG 418
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                                                                                                                                           247 GKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKVDEKPE-- 304
                                                                                              Gaps
                                                                                                                                                                                           3 GETTTEAVDAATAEKVFKQY-----ANDNG------VDGEWTYDDATKTFTVTEKPEVI 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 19, Last annotation update)
CELL SURFACE PROTEIN PRECURSOR.
Streptococcus equi subsp. zooepidemicus.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 EPTTAFIREAVREINQLSDDYADNOELQAVLAN-----AGVEALAADTVDQA--KA
                                                                                            20;
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                                                                                         27; Indels
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44830 MW; 270D43F92C197BBA CRC64;
114BAD7B500E3F62 CRC64;
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Pred. No. 3.8e-16;
                                          Score 670; DB 2;
Pred. No. 1.1e-25;
8; Mismatches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1
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Jonsson H., Lindmark H., Guss B.;
Zooepidamicus.";
Infect. Immun. 63:2968-2975(1995).
EMBL; U25852; AAA86832.1; -.
HSSP, P06654; IFCC.
InterPro; IPR002988; GA.
InterPro; IPR00724; IgG_bind_B.
InterPro; IPR00724; IgG_bind_B.
Pfam, PF01468; GA; I.
Pfam, PF01478; IgG_binding_B; 2.
Pfam, PF01378; IgG_binding_B; 2.
Pfam; PF01378; IgG_binding_B; 2.
PRINTS: PR00015; GPSANCHOR.
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39.6%;
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71.8%;
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                                                                                              Conservative
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Best Local Similarity
                                                                        Local Similarity
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96.6%;
                                                                                                                 298 VWTYDDATKTFTVTEM 313
                                                                                                     VWTYDDATKTFTVTEM 434
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                                                                                                                                                                                   PRELIMINARY;
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Best Local Similarity
Matches 56; Conserv
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                                                                              254 QIFRDYANKNGVDGVWAYDAATKIFTVTEQPVAETIEAAELIFPALTTYRLVIKGVTFSGE 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----AFSELKD 132
141 DAASVDQVNAAIN----DAHTAIADITGA---ALLEAKEAAINELKQYGISDYYVTLINK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 AVVNAEESTVSPVIVATDAVT------TSKEALAIINKLSEDN 66
                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                   ----NIRFAGKKVDEKPEEP-MDTYKLILNGKTLKGETTTEAVDAATAE
                                                                  335 KVFKOYANDNGVDGEWTYDDATKTFTVTEKP--EVIDASELTPAVTTYKLVINGKTLKGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 AQLKAYEDLAKLAADTDLDLDVAKIINDYTTKVENAKTAEDVK-----KIFFESQNEVT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239 KANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 413;
                                                                                                                                                                                                                                                                                                                                               MEDLINE-94259307; PubMed-7515368;
Jonsson H., Frykberg L., Rantamaeki L., Guss B.;
"MAG, a novel plasma protein receptor from Streptococcus
dysgalactiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F04DC71044F9E50F CRC64;
                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                        Gene 143:85-89(1994).
EMBL, 127798; AAA26921.1; -.
EMBL, 127798; AAA26921.1; -.
HISSP: P06654; 1PGA.
InterPro; IPR001298; GA.
InterPro; IPR00124; 1gG_bind_B.
Pfam; PF01468; GA: 1.
Pfam; PF01468; GA: 1.
Pfam; PF01378; IgG_binding_B; 1.
PRINTS; PR0015; GPOSANCHOR; 1.
PRINTS; PR00145; GRAM_POS_ANCHORING; UNKNOWN_1.
                                                                                                               393 TTTKAVDAETAEKAFKQYANDNGVDGVWTYDDATKTFTVTE 433
                                                                                                                            18.1%; Score 404; DB 2; L 32.3%; Pred. No. 1.9e-12; Live 31; Mismatches 110;
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                                                                                                                                                                                              PRELIMINARY;
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01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
MAG PROTEIN PRECURSOR.
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                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1334;
                     287 GYTI----
                                                                                                                                                                                                                                                                                                      Streptococcus.
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                                                                                                                                                            299 VDEKPEEPMDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATKT 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pteryyota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;

Sphingiodea; Sphingidae; Sphinginae; Manduca.

NCBI_TaxID=7130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-9377681; PubMed=8503988;
Cai S.Y., Wang Y.Y., Yao Z.J.;
"Structure analysis of streptococcal protein G Fc binding domain.";
Sci. China B 36:75-80(1993).
EMBL; S62801; AABZ7024.1; --
HSSP; P06654: 1PGX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58
                                                                                                                           359 FTVTEKPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           377 VTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVWTYDDATKTFTVTEM
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Pfam; PF01378; IgG_binding_B; 1.
SEQUENCE 60 AA; 6655 MW; 924567E0D6B513DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DBC-2001 (TEMBLrel. 19, Last annotation update)
PROTEIN G IGG FC BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 294; DB 2;
Pred. No. 4.2e-08;
1; Mismatches 1.
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EMBL: AF078161; AAF04457.1; -.
HSSP; P12111; ZKNT.
InterPro; IPR004094; Antistasin.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 AA.
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"The Bap Homolog Protein of Staphylococcus epidermidis RP62A Promotes
Biofilm Formation.";
                                                                                                                                                                                                                                                                                                                                                                                                      59 DNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEAT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 AEAYRYA-DALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QTAEFKGTFEEATAE-----AYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTP 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230 EEPKEEV-TIKANLIYADGKTQ-----TAEFKGTFAEATAEAYRYADLLAKENGKYTADL 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              284 EDGGYTINIRFAGKKVDEKPEEPMDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYAND 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----MRLEGKKLDEDASR------KTQQSTES--AADKAHETKDSVAQ 381
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                           ENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGFFEKATSEAYAY----ADTLKK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELKDSAVDTAKRAMGFLSGKTEETKQKAVETKDTAKEKMDEAGEEARRKMEE-----
  Nyakatura G., Fartmann B., Dauner D., Sterr W., Holland R., Welchselgartner M., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.,
                                                                                                                                                                                                                                                                                       Length 479;
                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                         EU Arabidopsis sequencing project;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL132969; CAB86908.1; -.
InterPro; PRO2987; LEA.
Ffam; PF02987; LEA.
SEQUENCE 479 AA; 52084 MW; C39E000D910E2385 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY028618; AAK29746.1; -. InterPro; IPR001298; Fllamin. InterPro; IPR001899; Gram_pos_anchor. InterPro; IPR0018019; HYR.
                                             Quetier F., Salanoubat M.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                   8.1%; Score 182; DB 10;
24.1%; Pred. No. 0.11;
tive 59; Mismatches 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium gro
Bacillus/Staphylococcus group; Staphylococcus
NCBI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  439 RPGYVATVLKEADQMTGQTFNDVG----EIDDEEK 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------ETAEKAFKQYANDNGVDGVWTYDDATK 427
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Matches 110; Conservative
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                                                                                       [2]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1076 -SEEITTEMTVTEETSETSPTEGTSDKTTMSTVSEETESS---SVTEETTTETTVVENAT 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1234 ----TEEPTDVGS-SEAITSDKTTVSTASEETGKYSVSEEE---TVKTTVAEASTEPSS 1284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 KGYTLNIKFAGKEKTPE-EPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAYRYADAL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    351 TYDDATKTFT---VTEKPEVID-ASELTPAVT--TYKLVINGKTLKGETTTKA---VDAE 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P8J2_210.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 TPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKAT-SEAYAYADTLKKDNGEYTVDVAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 KKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 YADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKVDEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 ATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEE-----PKEEVTIKANLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304 EEPMDTYKLILN-----GK-----TLKGETTTEAVDAATAEKVFKQYANDNGVDGEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                    Immunoglobulin domain; Serine protease inhibitor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                          349364 MW; AB4ACD459C0D9134 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
LATE EMBRYOGENESIS ABUNDANT PROTEIN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 23.4%; Pred. No. 0.97;
Matches 106; Conservative 71; Mismatches 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                     8.2%; Score 182.5; D
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                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                          PROSITE; PSO0317; 4_DISULFIDE_CORE; 1.
PROSITE; PSO0230; BPTI_KUNITZ_1; 8.
PROSITE; PSS0279; BPTI_KUNITZ_2; 10.
PROSITE; PSS0092; TSP1; 1.
InterPro; IPR002223; Kunitz_BPTI
                                                        Pfam; PP02822; Antistasin, 4. Pfam; PP00047; ig; 2. Pfam; PP000147; ig; 2. Pfam; PP000045; wap; 1. PRINTS; PR00759; BASICPTASE. SMART; SM00409; iGc2; 2. SMART; SM00209; TSP1; 7. SMART; SM00209; TSP1; 7.
                                          IPR002221; WAP
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                                                                                                                                                                                                                 SMART; SM00209; TSP1; 7. SMART; SM00217; WAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 3198 AA;
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SEQUENCE FROM N.A.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CELL ENVELOPE-ASSOCIATED PROTEINASE.
                                                                                                                                                          7.8%; Score 175; DB 10;
24.5%; Pred. No. 0.23;
ative 50; Mismatches 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1849 AA
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                                                                                                                               48492 MW;
                                                                     (MAR-2000) to the
                                                                                   EMBL; ACO06282; AAD20140.1;
InterPro; IPR004238; LEA.
Pfam; PF02987; LEA; 4.
SEQUENCE 448 AA; 48492 MA
                                                                                                                                                                        Best Local Similarity 24.5
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lactobacillus helveticus
 Nature 402:761-768(1999)
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                         SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
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MEROPS; S08.018; -.
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                                                                        Submitted
                                                                                                                                                            Query Match
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                                                           Lin X.
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MEDLINE-20083487; PubMed=10617197;
MEDLINE-20083487; PubMed=10617197;
Lin X., Kaul S., Rounaley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.W., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Omayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                          966 PDGVTFDEAT------NTISGTPSEVGSYDVTV----TTTDESGNSETTFFI 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1009 EVKDTT---KPTVESVADQTQEVNTEIEPIKIEARDNSGQAVTNKVDGLPDGVTFDEATN 1065
                                                                                                                                                                                                                                               156
                                                                                                                                                                                                                                                                          847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ILNGKTLKGETTTEAVDAATAE----KVFKQYANDNG-----VDG---EWTYDDATK 357
                                                                                                 Gaps
                                                                                                                                                                                    61 GE----YTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKG--- 112
                                                                                                                                                                                                               GDNVSPAITISVIDK -- TPPAVKAISNKTOKVNTEIEPIKIEATDNSGQAVTNKVEGLPA 789
                                                                                                                                                                                                                                                                                                      PEEPKEEVTIKANLIYADGKTQTAEFKG----TFEEAT-----AEAYRYADLLAK 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                         672 TTEDTSIKGTAEVDTNINLTFNDGRTLNGKVDSNGNFSIAIPSYYVLTGKETIKITSIDK 731
                                                                                                                                                                                                                                                                                                                                                                                TPETPETDSEEEVTIKANLIFANGSTQT - - AEFKGTFEKATSEAYAYA - - DTLK - - - KDN
                                                                                                                                                                                                                                              113 --TFEEAT-----AEAYRYADALKKDNGE----YTVDVADKGYTLNIKFAGKEKT
                                                                                                                                                                                                                                                                      790 GMTFDEATNTISGTPSEVGSYDITVTTTDENGNSETTTFTIDVEDT -- TKPTVESVADQT
                                                                                                                                                                                                                                                                                                                      ENGK - - - - YTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKG -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----TFTV----TEKPEVIDASELTPAVTT--YKLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 147;
                                                                     Length 2402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |: ||| |:|| | :|
-----GLPDGV-TFDETTNTISGT 1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INGKTLKGETTTKAVDAETAEKAFKQYANDNGV-DGVWTYDDATKTFTVT 432
          PROSITE; PS50194; FILAMIN REPEAT; 2.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
SEQUENCE 2402 AA; 258095 MW; D5807D96BBF2E9CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NY-2000 (TrEMBLrel. 13, Created)
NY-2000 (TrEMBLrel. 13, Last sequence update)
NY-2001 (TrEMBLrel. 19, Last annotation update)
EMBRYOGENESIS ABUNDANY PROTEIN (ATECP63).
                                                                     DB 2;
                                                                                    ; Pred. No. 1.2; 49; Mismatches 205;
                                                               Score 177.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
Pfam; PF00746; Gram_pos_anchor; 1.
                                                                    7.98;
                                                                                   Best Local Similarity 24.3% Matches 129; Conservative
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01-MAY-2000
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AT2G36640.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 RYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEF 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KGTFEEATAE------AYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPE 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGYTINIRFAGKKVDEKPEEPMDTYKLILNGKTLKGETTTEAVDAAT-----AEKV 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----NMEKAGEVTRQKMEE-----MRLEGKELKEEAGAKAQEASOKTRESTESGAQKA 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --FKQYANDNGVDGEWTYDDATKTFTVTEKPEVIDASEL------TPAVTTYKL 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 YTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----DYAVDKA-----VEAKDKTAEKAKETANYTADKA-KEAKDKTAEK 204
                                                                                                                                                                                                                                                                                                                                                                                                        3 ENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae; Lactobacillus.
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"Genetic characterization of a cell envelope-associated proteinase from Lactobacillus helveticus CNRZ32.";
J. Bacteriol. 181.4592-4597(1999).
EMBL; AF133727; AAD50643.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  205 VGEYKDYTVDKAVEARDYTAEKAIEAKDKTAEKTGEY-----KDYTVEKATEGKDVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259 KLGELKDSAVETAKRAMGFLSGKTEEAKGKAVETKDT------AKE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---EPKEEV--TIKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLED
                                                                                                                                                                                                                                                                                                                           Indels 142;
                                                                                                                                                                                                                                             Length 448;
EMBL/GenBank/DDBJ databases
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                                                                                                                                                           C72563D4194DD9BF CRC64;
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Local Similarity
               Best Local Sin
Matches 110;
  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :1:1 : | | | : | | | 1
                                                                                                                                                                                                                                     1415 TLNL---DSENTVYTNKDKFTI-SGTISDDYKFYDLSINGNDVETSWSAVDYHSKEGIKK 1470
                                                                                                                                                                                                                                                                                   218
                                                                                                                                                                                                           73 TLNÍKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA--YRYADALKK 130
                                                                                                                                                                                                                                                                 131 DNGEYTVDVADKGYTLNIK------FAGKEKTPEEPKEE--VTIKANLIYA 173
                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                     174 DGKTQTAEFK-----GTFEEATAEAYRYADLLAKENGKYTVDVADKGY-----TL
                                                                                                                                                                                                                                                                                                                                               1530 KATTDESEAKVVYSLDNGKTFNDVPADGFK -----VTENGTVQFKAVDK-YGNESKVKSV
                                                                                                                                                                                                                                                                                                                                                                            NIKFAGKEKTPEEPKEEVTIKANL---IYADGKTQ----TAEFKGTFAEATAEAYRYADL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      331 ATAEKVFKQYANDN-----GVDGEWTY-----DDATKTFT------VTEKP---
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                                                                                                                                                                                 125;
                                                                                                                                                      Length 1849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cucarella C., Solano C., Valle J., Amorena B., Lasa I I.,
Penades J.R.;
                                                                                                                                                                                 Indels
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EMBL; AF288402; AAK38834.1; -.
SEQUENCE 2276 AA; 238792 MW; 8623C60472CB0C0F CRC64;
                                                                                                                           219F0D44B15A091F CRC64;
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Last annotation update)
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Bacillus/Staphylococcus group; Staphylococcus.
NCBL_TaxID=1280;
                                                                                                                                                                                44; Mismatches 165;
                                                                                                                                                      DB 2;
                      * Pfam; PF02225; PA; 1.
Pfam; PF00082; Peptidase_S8; 3.
PRINTS; PROOF23; SUBTILISIN.
PROSITE; PS00136; SUBTILASE_ASP; UNKNOWN_1.
PROSITE; PS00136; SUBTILASE_ASP; UNKNOWN_1.
PROSITE; PS00137; SUBTILASE_HIS; 1.
PROSITE; PS00138; SUBTILASE_EIN; 1.
SEQUENCE 1849 AA; 199614 MW; 219F0D44BISA
                                                                                                                                                     7.6%; Score 170.5; I
25.9%; Pred. No. 1.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 399 DAETAEKAFKQYA------NDNGVD 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21189316; PubMed=11292810;
InterPro; IPR003137; PA.
InterPro; IPR000209; Peptidase_S8.
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                                                                                                                                                                 Best Local Similarity 25.9% Matches 117; Conservative
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093TY6;
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                                                                                                                                                                                                                                                                                                                                                                                                                         -------EEVTIKANLIYADGKTQTAEFKGTFEEATAEAYRYADLLAKENGKY 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKPEVIDASELT-PAVTT-----YKLVI--NGKTLKGE---TTTKAVDAETAEKA 406
                                                                                                                                                                                                               68 ADK-----GYTLNIKFAGKEKTPEEPK--------EEVTIKANLIYADGKTQT 107
                                                     Gaps
                                                                                                         8 TPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1599 PSNGDLNGGEELQVTATDKDGNTSEPSSANVTDTTASDAPTVNDVTSDATQVTGQAEPNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 TVDVADK-----EVTILNIKFAGKEKTPEEPK-------EVTIKANLIYADG
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                                                                                                                                                                                                                                                                                                                      108 AEFKGTFEEATAEAYRYADALKKDNGEYTVDVADK-----GYTLNIKFAGKEKTPEEPK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248 KTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLE-----DGGYTINIRFAGKKVDEK
                                                     Indels 150;
7.6%; Score 170; DB 2; Length 2276; 21.8%; Pred. No. 2.6;
                                                     197;
                                                     47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: October 29, 2002, 09:31:00 Job time : 35.364 secs
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October 29, 2002, 09:25:41; Search time 20.636 Seconds (without alignments) 2556.865 Million cell updates/sec
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1565
1 AVENKEETPETPETDSEEEV......GGYIINIRFAGKKVDEKPEE 305
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:* sp_vertebrate:*
sp_unclassified:*
sp_rvirus:* sp_bacteriap:* sp_archeap:* sp_plant:*
sp_rodent:* sp_virus:* SPTREMBL_19:* 10: Database :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	Q53291 streptococc	Q51912 peptostrept	Q51918 peptostrept	053975	Q91f88 arabidopsis	Q93em8 streptococc				Q91255 petromyzon			Q9u459 plasmodium	•	Q9u8g8 manduca sex	09jyk4 neisseria m
SUMM	Ω	053291	051912	051918	053975	Q9LF88	Q93EM8	Q9SKP0	096246	093TY6	091255	Q9S4K2	O9WZA6	090459	053837	Q9U8G8	Q9JYK4
	DB	~	~	7	7	10	7	10	10	7	13	7	16	2	7	Ŋ	16
	Duery Match Length DB	455	719	992	664	479	699	448	448	2276	1110	1849	992	5458	909	3198	737
dР	Ouery Match	100.0	99.7	78.4	10.7	10.6	10.6	9.6	9.5	9.5	9.0	9.0	8.8	8.8	8.7	8.6	8.5
	Score	1565	1561	1226.5	167	166	166	151	149	148.5	141.5	141	137.5	137.5	136	134.5	132.5
	Result No.	ч	2	m	4	S	9	7	80	6	01	11	12	13	,14	15	16

095ym2 procambarus 004111 enterococcu 086489 staphylococ 069188 streptococc 033742 streptococc	Q9kk48 streptococc Q99w46 staphylococ Q932f7 staphylococ Q9ki14 staphylococ Q9kwx6 staphylococ	0927r4 listeria in P87344 theragra ch Q9rqt5 streptococc 09ey85 clostridium 09482 neisseria q	047802 enterococcu 013099 xenopus lae 021380 caenorhabdi Q9a0K5 streptococc Q45574 bacillus sp Q9m9s5 arabidopsis	Q25920 plasmodium Q25921 glycine max Q9n435 caenorhabdi Q45547 mycoplasma Q99wg8 staphylococ Q55834 salmonella O96449 phytophthor
5 Q95xM2 2 Q04111 2 Q86489 2 G69188 2 O33742 2 O30874	2 Q9KK48 16 Q99W46 16 Q932F7 2 Q9KI14 2 O9KWX6		6 9	5 025920 10 039871 2 049835 2 049547 16 099WG8 2 053834 10 096449
17352 891 1166 564 581 663	701 1141 1141 1733 1733	938 1119 701 717	943 913 1035 2045 955 673	1510 463 2083 1302 495 506 1489
888888 7.44.6.6.6.		88888	88 88 88 11 11 11 11 11 11 11 11 11 11 1	88.0 0.88.0 0.9.7 0.9.0 0.9.0
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17 18 19 20 21 22	23 24 26 27	7 7 0 0 8 . 7 7 8 8 8 8 8 8	33 34 35 36 37	39 44 44 44 54

ALIGNMENTS

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NCBI_TaxID=1260;
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395 KPEE 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90215984; PubMed=2108927;
Kastern W., Holst E., Nielsen E., Sjobring U., Bjorck L.;
"Protein L. a bacterial immunoglobulin-binding protein and possible
virulence determinant.":
                                                                                                           AYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTA
                      EFFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKA
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Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
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BIDLINE-92316971; PubMed-1618782;

Bjoerck L., Sjoebring U., Kastern W.;

Bjoerck L., Sjoebring U., Kastern W.;

Structure of peptostreptococcal protein L and identification of repeated immunoglobulin light chain-binding domain.";

J. Biol. Chem. 257:12820-12825(1992).

EMBL; M86697; AAAA35612.1;

InterPro; IPR003147; B1.

InterPro; IPR001899; Gram_pos_anchor.
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Last annotation update)
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Matches 304; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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Pfam; PF00746; Gram_pos_anchor; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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EKPEE 326
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299 EYTVDVADKGLTLAIKFAGKKERPEEPREEVTIKVNLIFADGKTQTAEFKGTFEEATAKA 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murphy J.P., Trowern A.R., Duggleby C.J.;
"Nucleotide sequence of the gene for peptostreptococcal protein L.";
DNA Seq. 4:559-268(1994).
EMBL; L04466; AA467503.1; -.
HSSP; Q51911; 1GAB.
180 AEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKE--KTPEEPKEEVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 EYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA
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Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
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25 992 PROTEIN L.
992 AA; 108700 MW; 9CFF5771578A5DCE CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                 992 AA
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Interpro: IPR002988; GA.
Interpro: IPR001899; Gram_pos_anchor.
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Pfam; PF01468; GA; 4.
Pfam; PF00746; Gram_pos_anchor; 1.
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MEDLINE=95078460; Pubmed=7987012;
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051918;
01-NOV-1996 (TEMBLEEL 01, 01, 01-NOV-1996 (TEMBLEEL 01, 01, 01-DEC-2001 (TEMBLEEL 19,
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                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY).
-!- SIMILARITY).
-!- SIMILARITY).
-!- SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS IN THE REGION OF THE MEMBRANE ANCHOR. C-TERMINAL IS SIMILAR TO OTHER STREPTOCOCCAL TYPE-III FC RECEPTORS.

EMBL: Z29666; CAA82764.1; -.
HSSP: P06654; IPCX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 X 5 AA REPEATS OF [DEVP]-[DE]-[AT]-K-K.
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                Jonsson H., Mueller H.-P.; "The type-III Fc receptor from Streptococcus dysgalactiae is also an
                                                                                                                       Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
IMMUNOGLOBIN G BINDING PROTEIN MIG PRECURSOR (IGG BINDING PROTEIN
                                                                                                                                                                                                                                                                          Vasi J., Svensson J., Frick I.-M., Mueller H.-P.;
"Five homologous repeats of the protein G-related protein MIG cooperate in binding to goat immunoglobulin G.";
Infect. immun. 67:413-416(1999).
-!- FUNCTION: BINDS TO THE CONSTANT FC REGION OF IGG WITH HIGH AFFINITY. N-TERMINUS MEDIATES BINDING TO PLASMA PROTEINASE INHIBITOR ALPHA 2-MACROGLOBULIN AFTER COMPLEX FORMATION WITH
                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. CELL WALL (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMUNOGLOBIN G BINDING PROTEIN MIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pfam; PF00746; Gram_pos_anchor; 1.
Prfam; PF01718; IgG_binding_B; 5.
PRINTS; PR00015; GPOSANCHOR.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
PROSITE; PS00430; TONB_DEPENDENT RRC_1; UNKNOWN_1.
IgG-binding protein; Repeat; Transmembrane; Cell wall; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLUIAR (BY SIMILARITY).
MEMBRANE ANCHOR (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 X 24 AA REPEATS.
1-1.
1-2.
5 X 70 AA TANDEM REPEATS
(IGG CONSTANT REGION-BINDING).
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4A41CEEF7977862A CRC64;
                      664 AA.
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InterPro; IPR000724; IgG_bind_B.
InterPro; IPR000531; TonB_boxC.
                                           Created)
                                                                                                                                                                                                                      alpha 2-macroglobulin receptor.";
Eur. J. Biochem. 220:819-826(1994)
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5 x .
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                                                                                                                                                                 SEQUENCE FROM N.A., AND FUNCTION
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                                                                                                          Streptococcus dysgalactiae.
                     PRELIMINARY;
                                          01-NOV-1996 (TrEMBLrel.
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659
664
189
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639
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349
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01-JUN-2001
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TRANSMEM
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REPEAT
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                   053975
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                                                                                      MIG).
RESULT 4
          053975
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Length 664;

DB 2;

Score 167; DB Pred. No. 0.08;

10.78; 27.48;

Query Match Best Local Similarity

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12;
     16;
                                                                                                                                                                                -YADALKKDNGEYTVDVADKGYTLNIKFA---GKEKTPEEPKEEVTIKANLIYADGKTQT 179
                                                                                                                                                                                                                                                                                  AEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFA---GKEKTPEEPKEEV 236
                                                                                                                                                                                                                                                                                                                                                                                     438 IVKGNTF--SGETTT---KAVDAETAEKAFKQ---YANENGVY-----GEWSYDDATKT 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                   VADKGYTLNIKFA---GKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAYR 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 QTAEFKGTFEEATAE-----AYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTP 229
  40; Gaps
                                                   ETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVD 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K.F.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 166; DB 10; Length 479;
; Pred. No. 0.062;
43; Mismatches 137; Indels 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

Nyakatura G., Fartmann B., Dauner D., Sterr W., Holland R.
Weichselgartner M., Mewes H.W., Rudd S., Lemcke K., Mayer:
Quetier F., Salanoubat M.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
  Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EU Arabidopsis sequencing project;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AL132969; CAB86908.1; -.
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Pfam; PF02987; LEA; 5.
SEQUENCE 479 AA; 52084 MW; C39E000D910E2385 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
LATE EMBRYGGENESIS ABUNDANT PROTEIN-LIKE.
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49;
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(TrEMBLrel. 15, I
(TrEMBLrel. 19, I
     Conservative
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Matches 82; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          484 FTVTEKP 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297 KKVDEKP 303
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01-0CT-2000
  84;
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SEQUENCE
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214 DAPELTPALTTYKLVVKGN-TFSGETTTKAIDTATAEKEFKQ-YATANNV---DGEWSYD 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 VADKGYTLNIKFA---GKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA-- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269 DATKTFTVTEKPAVIDALELTPALTTYKLIVKGNTF--SGETTTK----AIDAATAEKEF 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 YRYADALKKDNGEYTVDVADKGYTLNIKFA---GKEKTPEEPKEEVTIKANLIYADGKTQ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 TAEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFA---GKEKTPEEPKEE 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      380 TKAIDAATAEKEFKOYATAN---NVDGEWSYDDATKTFTVTEKPAVIDAPELTPALTTYK 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 VTIKANLIYADGKTQTAEFKGTFAEATAEAYR-YADLLAKENGKYTADLEDGGYTINIRF 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                437 LIVKGNTF--SGETTT---KAVDAETAEKAFKQYA------TANNVDGEWSYDDAT 481
                                                                                                                                                                                                                                                                                                                                                                                                                       44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         7 ETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVD 66
                                                                                                                                                                                                          Streptococcus dysgalactiae.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                       STRAIN=ATCC 43078;

BELLINE-21437603; PubMed-11553540;
Song X.M., Perez-Casal J., Bolton A., Potter A.A.;
"Surface-Expressed Mig Protein Protects Streptococcus dysgalactiae against Phagocytosis by Bovine Neutrophils.";
Infect. Immun. 69:6030-6037(2001).
EMBL; AF354651; AAL09476.1; -.
                                           230 EEPKEEV-TIKANLIYADGKTQ----TAEFKGTFAEATAEAYRYADLLAKENGKYTADL
                                                                                                                                                                                                                                                                                                                                                                                                 Length 669;
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                                                                                                                                                                                                                                                                                                                                                                           5C8982B952029B03 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                      48; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
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72682 MW;
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------MRLEGKKLDE 355
                                                                      284 EDGGYTINIRFAGKKVDE 301
                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 27.5% nes 85; Conservative
                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                           669 AA;
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                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          NCBI_TaxID=1334;
                                                                                                                                                                                                MIG PRECURSOR
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01-MAY-2000
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Q9SKP0;
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SIGNAL
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Q93EM8
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SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
STRAIN=CV. COLUMBIA;
MEDLINE=20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                         Buabidopsis thaliana (Mouse-ear cress).
Bukaryopt; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosida II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 YTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 VGEYKDYTVDKAVEARDYTAEKAIEAKDKTAEKTGEY-----KDYTVEKATEGKDVTVS 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATECP63.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae. Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons; core eudicots; Rosidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 KLGELKDSAVETAKRAMGFLSGKTEEAKGKAVETKDT-----AKEN------MEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 Y-----KDYTVDKAKEAKDTTAEKAKETANYTADKA-VEAKDKTAEKIGEYK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 RYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C72563D4194DD9BF CRC64;
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
LATE EMBRYOGENESIS ABUNDANT PROTEIN (ATECP63).
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Last annotation update)
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24.5%; Pred. No. 0.38;
Live 38; Mismatches 107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87; LEA; 4.
448 AA; 48492 MW;
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19,
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Matches 79; Conservative
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01-FEB-1997 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
LEA PROTEIN IN GROUP 3.
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1685 PSNVDLNGGEELQVTATDKDGNTSEPSSANVTDTTAPDAPTVNDVTSDATQVTGQAEPNS 1744
                                                                                                                                                                                                                                                                                             1853 TIDIPSNVDLNGGEELQVTATDKDGNTSEPSSANVTDTTAPDAPTVNDVTSDATQVTGQA 1912
                                                                                                                                                                                                                               1799 TNVTDTTASDAPTVNDVTSDASQVTGQAEPNST-VKLTFPDGTT-----ATGTADDQGNY 1852
                                 -----AD----DQGNYTIDI 1684
                                                                                                                                108 AEFKGTFEEATAEAYRYADALKKDNGEYTVDVADK-----GYTLNIKFAGKEKTPEEPK- 161
                                                                                                                                                                                                ------EEVTIKANLIYADGKTQTAEFKGTFEEATAEAYRYADLLAKENGKY 207
                                                                 ----EEVTIKANLIYADGKTOT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 NGEYTVDVADKGYT------LNIKFAGKEKTPEEPKEEVTIKANLIYADGKT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QTAEFKGTFEEATAEA-----YRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEE--PKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAYRYADLLAKENGKYTVDVADK 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AVENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFE-KATSEAYAVADTLKKD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----EEVTIKANLIYADG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EAAEAKAEVEEEEAEBEEEEEEAEEEEVEAETKEEVEAEAEVEEEGE------AAEEEA
   TPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Petromyzon marinus (Sea lamprey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
NCBI_TaxID=7757;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jacobs A.J., Kamholz J., Selzer M.E.;
The single lamprey neurofilament subunit (NF-180) lacks
multiphosphorylation repeats and is expressed selectively in
projection neurons.";
Brain Res. Mol. Brain Res. 29:43-52(1995).

EMBL; U19361; AAA80106.1; -.
InterPro; IPR00164; IF.
InterPro; IPR00164; Ir.
Prints Pro0194; Tropomyosin.
Pram; Pr00194; Tropomyosin.
PROSITE; PS001296; IF; UNKNOWN.1.
SEQUENCE 1110 AA; 123818 MW; 6558DA73DAF6974C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           selectively
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                    248 KTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGG 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138;
                                                                                                                                                                                                                                                                                                                                                                                                                                               AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.0%; Score 141.5; I 25.4%; Pred. No. 3.6; rative 38; Mismatches
                                 1644 TSDATQVTGQAEPNSTVKLTFPDGTTAT----GT---
                                                                                                                                                                                                                                                               208 TVDVADK----GYTLNIKFAGKEKTPEEPK---
                                                                 ADK - - - - - GYTLNIKFAGKEKTPEEPK - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 YTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----DYAVDKA------VEAKDKTAEKAKETSNYTADKA-KEAKDKTAEK 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 KGTFEEATAE-----AYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPE 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205 VGEYKDYTVDKAVEARDYTAEKAIEAKDKTAEKTGEY-----KDYTVEKATEGKDVTVS 258
                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        123 RYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEF 182
                                                                                                                                                                                                                                                                                                           ENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97;
                                                           STRAIN-COLUMBIA; TISSUE-DRY SEED;
MEDLINE-97169149; PubMed-9016956;
Yang H., Saitou T., Komeda Y., Harada H., Kamada H.;
"Arabidopsis thaliana ECP63 encoding a LEA protein is located chromosome 4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2276;
                                                                                                                                                                                                                                            DB 10; Length 448;
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"Bap, a Staphylococcus aureus Surface Protein Involved in Formation.",
                                                                                                                                                                                                                                           9.5%; Score 149; DB 10; Length 4 24.5%; Pred. No. 0.49; tive 38; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sucarella C., Solano C., Valle J., Amorena B., Lasa I I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Bacteriol. 183:288-2896(2001).
EMBL; AF288402; AAK38834.1; -
SEQUENCE 2276 AA; 238792 MW; 8623C60472CB0C0F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                              DC37099F18FBA85E CRC64;
Brassicales; Brassicaceae; Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
BIOFILM-ASSOCIATED SURFACE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.5%; Score 148.5; DB 2;
21.2%; Pred. No. 3.4;
ive 36; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus. NCBI_TaxID=1280;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGEVIROKMEEMRLEGKELKEE 324
                                                                                                                                         Gene 184:83 48 (1997).

EMBL: D64140; BAA11017.1; -.

InterPro; IPPR004238; LEA.

Pfam: PF02087; LEA; 4.

SEQUENCE 448 AA; 48534 MW;
                                                                                                                                                                                                                                                                           79; Conservative
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Best Local Similarity 21.2
Matches 72; Conservative
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                                             SEQUENCE FROM N.A.
               NCBI_TaxID=3702
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Matches
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STRAIN=FCC1/HN;
Shan Z.X., Yu X.B., Li X.R., Ma C.L., Fang J.M., Lu J.H., X J.;
"Molecular cloning and structure analysis of the Plasmodium falciparum
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MEDLINE=99287316; PubMed=10360571;
MEDLINE=99287316; PubMed=10360571;
MEDLINE=99287316; PubMed=10360571;
Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson D.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from Nature 399:323-329(1999).

Mature 399:323-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219 VLSKDETVEVSEKDIYQK-----NLLLKPGDTVHVQKIDERFAYVVGAVARPGMYTFSRE 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----EPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAYRYAD 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              379 VVTRDGSVITLS-----PNNLDFSVKPGDVVNVKEFVPKKA---YVLGYVRN---PGLY 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --EYTVDVADKGYTLNI-----KFAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         332 -EKTEVYVSGYVSRPGVYEISPKENVTLEKLLSMAGG-----IKGTLEEVD-----SI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ERYTHROCYTE MEMBRANE-ASSOCIATED GIANT PROTEIN ANTIGEN 332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 GKTQTAEFKGTFAEATAEAYRYADLL-----AKENGKYTADLED 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               992 AA; 109623 MW; 19291DDF29721BF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    477 GVEVYVE------RYTDRFVYMVGDNVSRNGKMSFEKEE 509
                                        Created)
Last sequence update)
Last annotation update)
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992 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40; Mismatches
                                                                                                      POLYSACCHARIDE EXPORT PROTEIN, PUTATIVE
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                                                                                                                                                                       Thermotogales; Thermotoga
                                     01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAX-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 090459; 09GPC4;
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
01-DEC-2001 (TrEMBLrel. 19,
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Matches 77; Conservative
PRELIMINARY;
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                                                                                                                                                   Thermotoga maritima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 KEKTPE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 TLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA--YRYADALKK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNGEYTVDVADKGYTLNIK------FAGKEKTPEEPKEE--VTIKANLIYA 173
                                                            ----VEAESKEEEEEDSKEADAEEDEAEEEEVKEEEVTKSDAEEAEAEEEEAAKSEEE 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-99350424; PubMed-10419958; Pederson J.A., Mileski G.J., Weimer B.C., Steele J.L.; "Genetic characterization of a cell envelope-associated proteinase from Lactobacillus helveticus CNRZ32."
                    -----EEVTIKANLIYADGKTQTAEFKGTFAEATAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIKFAGKEKTPEEPKEEVTIKANL - - - IYADGKTQ - - - - TAEFKGTFAEATAEAYRYADL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219F0D44B15A091F CRC64;
                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                            740 AAEEAKDEAEEEEAEEEAVEETEAATEEAEAKEASDDEKPEE 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.7%; Pred. No. 0..,
tive 32; Mismatches 108;
                                                                                                      265 AYRYA-DLLAKENGKYTADLEDGGYTINIRFAGKKVDEKPEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.0%; Score 141; DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1641 LADKNAK-LADLQDAAKALD--KAEQALTEKPAE 1671
                                                                                                                                                                                                                                                          PRT; 1849 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF02225; PA; 1.
Pfam; PF00082; Peptidase_S8; 3.
PRINTS; PR00723; SUBTILISIN.
PROSITE; PS00588; PLAGELLA_BB_ROD; UNKNOWN.
PROSITE; PS00136; SUBTILASE_ASP; UNKNOWN.1
PROSITE; PS00137; SUBTILASE_ASP; UNKNOWN.1
PROSITE; PS00138; SUBTILASE_BIS; 1.
SEQUENCE 1849 AA; 199614 WW; 219F0D44B
                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                   CELL ENVELOPE-ASSOCIATED PROTEINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Bacteriol. 181:4592-4597(1999).
EMBL; AF133727; AAD50643.1; -.
HSSP; P00782; 1SUC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000209; Peptidase_S8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001444; Flag_bb_rod InterPro; IPR003137; PA.
                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 13, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                 215 GYTLNIKFAGKEKTPEEPK
                                                                                                                                                                                                                                                                                                                                                                                                           Lactobacillus helveticus
                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel
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Matches 76; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEROPS; S08.018;
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01-DEC-2001
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DNGEYTVDVADK - - - GYTLNIKFAGKEKTPEEPKEEVTIKANLIYAD-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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432 ALRSDLGAVQNRFNSAITNLGNTVN 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLAKENG----KYTADLEDGGYTIN 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR003598; Ig_c2.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR00223; Kunitz_BPTI.
Interpro; IPR000884; TSPI.
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Pfam; PF00047; ig; 2.
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SMART; SM00408; IGC2; 2.
SMART; SM00131; KU; 10.
SMART; SM00209; TSP1; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; ig; 2.
Pfam; PF00014; Kunitz_BPTI;
Pfam; PF00095; wap; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19, LACUNIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR002221; WAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00217; WAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3198 AA;
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                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vanegas R.A., Joys T.M.; "Molecular analyses of the phase-2 antigen complex 1,2. . of Salmonella
                                                                                                                                                                                                                                                                                                                                                                     1985 VEQTDSVTEKVIEQEGSNTEVAEDVEEK------ESASDEHEQEDVSVNAQV--- 2030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKK-------DNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYAD 102
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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enythrocyte membrane-associated giant protein Ag332 (Pf332) gene."; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF202180; AAF15293.3; -
InterPro. IPR00113 PUM.
SEQUENCE 545R xx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2075 FATVTEEVVEDGSVIEEVVEDGSVIEEIVQENGSVIEEIVEEKSSN---
                                                                                                                                                                                                                                                           ENKEET --- PETPETDSEEEVTIKANLIFANGSTQTAEF ---- KGTFEKATSEAYAYADT
                                                                                                                                                                                                                                                                                                                                                                                                                    103 GKTQTAEFKGTFEEATAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 EVTIKANLIYADGKTQTAEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              223 AGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFAEATAEAY-RYADLLAKENGKYTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella cholerae-suis (Salmonella enterica).
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Salmonella.
                                                                                                                                                                                                                      67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118;
                                                                                                                                                                               Length 5458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 506;
                                                                                                                                                                             ; Score 137.5; DB 5; Length; Pred. No. 37; 55; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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24.4%; Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Pred. No. 2.9;
44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-SEROTYPE CHOLERAESUIS, ATCC 7001;
MEDLINE-95325331; PubMed=7541401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DL-EDGGYTIN-'IRFAGKKVDEKPEE 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Bacteriol. 177:3863-3864(1995).
EMBL; U17175; AAC43352.1; -.
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InterPro; IPR001492; Flagellin_N.
                                                                                                                                                                             8.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.48;
                                                                                                                                                                                                                    67; Conservative
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Best Local Similarity
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Matches 9
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SEQUENCE FROM N.A.
MEDLINE=99457716; PubMed=10528409;
Nardi J.B., Martos R., Walden K.K., Lampe D.J., Robertson H.M.;
Nardi J.B., artos R., alarge multidomain extracellular matrix
protein, accompanies morphogenesis of epithelial monolayers in Manduca
                                                                                                                                              230 EEPKEEVTIKANLIYADGKTQTA-----EFKG--TFAEATAE------AYRYAD 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102
                                                                                                                                                                                                                                                                                                                                                                                                 312 ANGAELVKMSYTDKNGKTIDGGYALKAGDKYYAADYDEATGAIKAKTTSYTAADGTTKTA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingidae; Sphinginae; Manduca.
                                264 TLA-AGATKT----TMPAG---ATTKTEVQELKDTPAVVSADAKNALIAGGVDATD
                                                                                                                -----GKTQTAEFKGTFEEATAEAYRY-----ADALKKDNGEYTVDVADKGYTL
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                                                                                                                                                                                                                              147 NIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA---
                                                                                                                                                                                                                                                                                                                                           -----YRYADLLAKE-NGKYTVDVADKGYTLNIKFA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 13, Last sequence update) (TrEMBLrel. 19, Last annotation update)
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SIGNAL 1 21 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insect Biochem. Mol. Biol. 29:883-897(1999).
EMBL; AF078161; AAF04457.1; -.
HSSP: P12111; 2KNT.
InterPro; IPR004094; Antistasin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 3198 AA.
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Pred. No. 30;
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24.8%;
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Best Local Similarity
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                      Qy <' 11 TPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKAT-SEAYAYADTLKKDNGEYTVDVAD 69
1028 TEESSVAEEETTK-----TITTEEVSGTSESASINSDKTTMTLLSEDTGKTSV--- 1075
                                                                                                                      70 KGYTLNIKFAGKEKTPE-EPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAYRYADAL 128
                                                                                                                                                                       189 ATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEE-----PKEEVTIKANLI 243
Matches 70; Conservative 39; Mismatches 126; Indels 47; Gaps
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Search completed: October 29, 2002, 09:30:54 Job time: 29.636 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

; Search time 7.42896 Seconds
(without alignments)
1589.653 Million cell updates/sec October 29, 2002, 09:25:26 Run on:

Title: Perfect score:

US-08-325-278B-1 1565 1 AVENKEETPETPETDSEEEV......GGYTINIRFAGKKVDEKPEE 305 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SwissProt_40:* Database :

	riptio	Q53654 staphylococ		-	salmone	P02565 gallus gall	rattus	P46821 homo sapien	_	P37575 bacillus su	P19909 streptococc	O33479 pseudomonas	P06620 pseudomonas		P80544 staphylococ	Q08641 saccharomyc	-		P12839 rattus norv				Q90339 cyprinus ca		_	Q04968 borrelia bu		P45387 haemophilus		P08799 dictyosteli		<u>-</u>	m.	P97794 mus musculu
SUMMARIES	QI 1	CNA_STAAU								SP2B_BACSU	SPG2_STRSP	. ICEV_PSESX		SSP5		_	_														SIAL	SLPO	_	IRK8_MOUSE
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	V34114 streptococc P48467 neurospora	Q53957 streptococc	Q62234 mus musculu	P12882 homo sapien	P05423 homo sapien	P16620 drosophila	P06176 salmonella	P13466 dictyostel1	Q28641 oryctolagus	P21333 homo sapien
YFI6_YEAST	YACY_STRED KINH_NEUCR	TACY_STRCB	MYM1_MOUSE	MYH1_HUMAN	BN51_HUMAN	PTP6_DROME	FLIC_SALCH	GELA_DICDI	MYH4_RABIT	ABP2_HUMAN
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111.5	110.5	109.5	109.5	109.5	109	109	108.5	108.5	108.5	108.5
34	36	37	38	39	40	41	42	43	44	45

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277 GKYTADLEDG 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           986 NCTITHKY----TPGETSATVTKNWDDNNNQDGKRPTEIKVEL-YQDGKATGKTAILN 1039
                                                                                                            CYTOPLASMIC (POTENTIAL).
COLLAGEN-BINDING.
3 x 187 aa APPROXIMATE TANDEM REPEATS.
LYS/PRO-RICH (CELL WALL-SPANNING).
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                                      ----- 752 762
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                                                                                                                                                                                                                                                                                                                                                                     816 VTKNWDDNNNQDGKRPTEIKVEL-YQDGKATGKTAILNESNNWTHTWTGLDEKAKGQQVK 874
                                                                                                                                                                                                                                                                                                                                                                                         124 Y-ADALKKDNGEYT-VDVADKG-----YT----LNIKFAGKEKTPEEPKEEVTIKAN 169
                                                                                                                                                                                                                                                                                                                                                                                                              934
                                                                                                                                                                                                                                                                                                                                                                                                                                  ----YTVDVAD 213
                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                  47
                                                                                                                                                                                                                                                                                                          91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Spermatophyta; Spermatophyta; Core eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus. NCBL_TaxID-4039;
                                                                                                                                                                                                                                                                  2 VENKEETPETPETDSE------EEVTIKANLIFANGSTQTAEFKGTFEKATS
                                                                                                                                                                                                                                                                                                          -----EYTVDVADKGYTLNIKFAGKEKTPEEPKEE
                                                                                                                                                                                                                                                                                                                                                  ---IKANLIYADGKTQ------TABFKGTFEEATAEAYR
                                                                                                                                                                                                                                                                                                                                                                                                            875 YTVEELTKVKGYTTHVDNNDMGNLIVTNKYTPETTSISGEKVWDDKDNQDGKRPEKVSVN
                                                                                                                                                                                                                                                                                                                                                                                                                                              -----TAEFKGTFAEATAEAYRY-ADLLAKENGKYTADLED----GGYTINIRFAGKKVD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 KGYTLNIKFAGKEKTPEEPKEEVT------IKANLIYADGKTQ-----
                                                                                                                                                                                                                                             159;
                                                                                                                                                                                                                           Length 1183;
                                                                                         EXTRACELLULAR (POTENTIAL). MEMBRANE ANCHOR (POTENTIAL).
                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                     713 VINK-YTPETISISGEKVWDDKDNQDGKRPEKVSV--NLLADGEKVKTLD-
                                                                                                                                                                                                       B6A1CC072E575D76 CRC64;
                          PDB; lAMX; 24-JUN-98.
Interpro; IPRO01899; Gram_pos_anchor.
PROSITE; PS00343; GRAM_POS_ANCHORING; FALSE_NEG.
Signal; Repeat; Transmembrane; Cell wall; 3D-structure.
                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                             123;
                                                                                                                                                                                                                                                                                                                                                                                                                                170 LIYADGKTQTAEFKGTFEEATAEA---YRYADLLAKENGK--
                                                                                COLLAGEN ADHESIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
30-MAX-2000 (Rel. 39, Last annotation update)
Embryonic protein DC-8 (Clone 8/10).
                                                                                                                                                                                                                         Score 151.5; DB Pred. No. 0.064; 5; Mismatches 1
or send an email to license@isb-sib.ch)
                                                                                                                                                                PROTEINS
                                                                                                                                                                                                       AA; 133066 MW;
                                                                                                                                                                                                                                                                                                          EA---YAYADTLKKDNG-----
                                                                                                                                                                                                                          9.78;
                  EMBL; M81736; AAA20874.1;
                                                                                                                                                                                                                                               Conservative
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1177
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                                                                                                                                                                                                      1183
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Matches 102;
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P20075;
                                                                                         DOMAIN
TRANSMEM
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
                                                                                                                                                                                      AND CELL WALLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DTTV---GKMTELKDSAADAARKAMDMFLGKKEEVKGKAGETAEAAKEKYEDTEFAARKK 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 OKAAEAKDTTAOKA-----AEAKEKTGEYKDYAAOKAAEAKVLAAOKAAEAKDTTG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72; Gaps
                                                                                                                            MOI. Gen. Genet. 218:143-151(1989).
-!- FUNCTION: MAY PLAY A ROLE IN LATE EMBRYOGENY.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC, PROTEIN BODIES, AND CELL WAI
-!- SUBCELLULAR LOCATION: AND ENDOSPERM TISSUE.
-!- SIMILARITY: SOME, TO COTTON LEA D7, TO RAPE LEA 76, AND CARROT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      277 KAKEYKEYAAQKAAEAKDATMQKTGEY-----KDYSAQKAAETKDATMEKTKE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYA-----DTLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 ATAEAYRYA------DALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKA
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                                                       Franz G., Hatzopoulos P., Jones T.J., Krauss M., Sung Z.R.; "Molecular and genetic analysis of an embryonic gene, DC 8, from Daucus carota L.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X APPROXIMATE TANDEM REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 141; DB 1; Length 555; Pred. No. 0.11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
STRAIN=CV. QUEEN ANNE'S LACE;
MEDLINE=89384429; PubMed=2571069;
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111.
112.
113.
114.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S04909; S04909.
InterPro; IPR004238; LEA.
Pfam; PF02987; LEA; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 25.2
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NLIYADGKTQTA--
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                                               --YKFSKHLK------AGEGYKMQ---SGDLKIPASQFENNHGYLLKVR 248
                                                                                                                                                                                                                                           309 INSYFFYDVYKTATNPFPSDEATFKODWNTWSGSEIDTQAVKDIVNQVHDGGAVAMLYNM 368
     113 TFEEATAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPE---EPKEEVTIKAN 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FORM THE FILAMENTS OF BACTERIAL FLAGELLA.

-!- MISCELLANEDUS: INDIVIDUAL SALMONBLLA SEROTYPES USUALLY ALTERNATE
BETWEEN THE PRODUCTION OF 2 ANTIGENIC FORMS OF FLAGELLA, TERMED
PHASE-1 AND PHASE-2. BACH SPECIFIED BY SEPRARATE STROUTURAL GENES.
-!- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                               170 LIYADGKTQTAEFKGTFEEATAEAY-RYA-------DLLAKENGKYTVDVAD-KGYT
                                                                                                                                            249 VRDADNNTLSEVNKAIAVESDWTKFPRYGIVGGSQDTNNSLLSKDADRYRAEIEKMKNMN
                                                                                                                                                                                              218 LNIKF----AGKEKTPEEPKEEVTIKANLIYADGK----TQTA-EFKGTFAEATAEAYRYAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE-8204941; PubMed-6271461; Simon M.; Sieg J., Mandel G., Simon M.; and the functional components of the phase variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vanegas R.A., Joys T.M.;
"Molecular analyses of the phase-2 antigen complex 1,2,...
                                                                                                                                                                                                                                                                                                                         :||: | :: | | :: | | 369 ILAENTNTGEAPVLPETEYAYNSDDRGYGAQGQPMSYTVKIPKDGQEED 417
                                                                                                                                                                                                                                                                                             271 LLAKENG------KYTADLEDGG-----YTINIRFAGKKVD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cold Spring Harb. Symp. Quant. Biol. 45:17-26(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mingorance J., Tanaka S., Tominaga A., Enomoto M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P52616; P97159;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   505 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=LT2 / SGSC1412 / ATCC 700720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteriol. 177:3863-3864(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95325331; PubMed=7541401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 482-505 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-37 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phase-2 flagellin.
FLJB OR H2 OR STM2771.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella spp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=SJ2353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FLJB_SALTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-SL
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                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
FLJB_SALTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Type I membrane protein. Cell wall.
SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS
IN THE REGION OF THE MEMBRANE ANCHOR.
SIMILARITY: BELONGS TO FAMILY 66 OF GLYCOSYL HYDROLASES.
CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-5 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 DNGEYTVDV-ADK-----GYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EETPETPET-DSEEEVTIKANLI--FANGSTQ----TAEFKGTFEKATSEAYAYADTLKK 58
                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=6715 / UMB66;
MEDLINE-94292401; PubMed-8021165;
WEDLINE-94292401; PubMed-8021165;
Wends S.-Y., Curtiss R. III;
Wends S.-Y., Curtiss Representation of Streptococcus sobrinus
dextranase produced in recombinant Escherichia coli and sequence
analysis of the dextranase gene.";
J. Bacteriol. 176:3839-3850(1994).
J. Bacteriol. 176:3839.
J. Bacteriol. 176:3839-3850(1994).
J. Bacteriol. 176:3839-3850(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase; Glycosidase; Signal; Transmembrane; Repeat; Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 130.5; DB 1; Length 1337; Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEMBRANE ANCHOR (BY SIMILARITY). CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.3%; Score 1.v....
22.9%; Pred. No. 1.2;
+ive 51; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MW; B494275A77A2E3D0 CRC64;
                                                                                                                                                                                         01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Dextranase precursor (EC 3.2.1.11) (Alpha-1,6-glucan-6-
                                                                                                                                                                                                                                                                                                                    Streptococcus downei (Streptococcus sobrinus)
                                                                                                                     1337 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 31-36.
STRAIN=6715 / UAB66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00746; Gram_pos_anchor; 1.
PROSITE; PS00343; GRAM_POS_ANCHORING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEXTRANASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M96978; AAA21772.1; -.
InterPro; IPR001899; Gram_pos_anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEINS
                                                                                                                   PRT;
                                                                                                                                                                01-FEB-1995 (Rel. 31, Created)
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                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1337 AA;
439 MEELKLQEEG 448
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                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus.
NCBI_TaxID=1317;
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                                                                                                                                                                                                                                                                                                                                        Plasmid pYA902
                                                                                                                   DEXT_STRDO
P39653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
TRANSMEM
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                                                                                               DEXT_STRDO
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J. Biol. Chem. 262:6478-6488(1987).
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ProDom; PD000355;
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                                                                                                                                                                                                                                         light meromyosin.
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   NAMES OF THE PROPERTY OF THE P
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   and for commercial
                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95 AVQSANSTNSQSDLDSIQAEITQRLNEIDRVSGQTQ---FNGV--KVLAQDNTLTIQVGA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 DNGEYTVDVADK---GYTLNIKFAGKEKTPEEPKEEVTIKANLIYAD-------- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150 NDGE-TIDIDLKQINSQTLGLDSLNVQKAYDVKDTAVTTKA---YANNGTTLDVSGLDDA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   311 ANGAELVKMSYTD----KNGKTIEGGYALKAGDKYYAADYDEATGAIKAKTTSYTAADGT 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              367 TKTAANQLGGVDGKTEVVTIDGKTYNASKAAGHDFKAQPELAEAAAKTTENPLQKIDAAL 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDIATE STATE STA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AVENKEETPETPETDS-EEEVTIKANLI-FANGSTQTAEFKGTFEKATSEAYAYADTLKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 -----GKTQTAEFKGTFEEATAEAYRY-----ADALKKDNGEYTVDVADKGYTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206 AIKAATGGTNGTASYTGGAVKFDADNNKYFVTIGGFTGADAAK--NGDYEVNVATDG-TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : || || || || 263 TLA-AGATKT-----TMPAG---ATTKTEVQELKDTPAVVSADAKNALIAGGVDATD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 -----YRYADLLAKENGK----YTVDVADKGYTLNIKFA-------GK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226 EKTPEEPKEEVTIKANLIYADGKTQTA-----EFKG--TFAEATAE-----AY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Watch 8.2%; Score 129; DB 1; Length 505; Local Similarity 24.2%; Pred. No. 0.51; les 94; Conservative 43; Mismatches 126; Indels 126;
   Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 NIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         I -> S (IN REF. 3).
3A5CC404AF7AF88B CRC64;
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01-FBB-1996 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, fast skeletal muscle, embryonic.
   modified and this statement is not removed.
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                                                            or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267 RYADLLAKENG----KYTADLEDGGYTIN 291
                                  entities requires a license agreement
                                                                                                                                              EMBL; AE008826; AAL21657.1; -.
EMBL; V01370; CAA24655.1; -.
EMBL. D26168; BAA05156.1; -.
StyGene; SG10564; f19B.
InterPro; IPR001029; Flagellin_C.
InterPro; IPR001492; Flagellin_N.
Pfam; PF00700; Flagellin_N.
                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00207; FLAGELLIN.
ProDom; PD000316; Flagellin_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 37 I
505 AA; 52404 MW;
                                                                                                                        EMBL; U17177; AAC43354.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Flagella; Complete proteome.
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P02565;
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CONFLICT
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                                                                                                                                                                                                               14. J. Biol. Chem. 228:5196-5205(1983).

15. T. SUBJUL. CHELDINYSALIN.

16. T. SUBJULT. MUSCLE CONTRACTION.

17. SUBJULT. MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBJULTS (MHC), 2 ALKALI LIGHT CHAIN SUBJULTS (MLC).

18. SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

19. SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

19. CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COLLED COLLS.

19. PPM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

20. MASCELLANBOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (HMM). IT CAN LATER BE SPLIT INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
SEQUENCE OF 1502-1940 FROM N.A.
MEDLINE=83161144; PubMed=6833296;
Kavinsky C.J., Umeda P.K., Sinha A.M., Elzinga M., Tong S.W., Zak R.,
Jakovcic S., Rabinowitz M.;
"Cloned mRNA sequences for two types of embryonic myosin heavy chains
from chick skeletal muscle. I. DNA and derived amino acid sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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SMART; SM00015; IQ, 1.
PROSITE; PS50096; IQ, 1.
Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; Calmodulin-binding; ATP-binding; Methylation; Alkylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1940;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBFRACMENT (S2).
SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 10 DOMAIN.
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T -> A (IN REF. 2).
ERA -> GRT (IN REF. 2).
MW; C34833D75B04DFF2 CRC64;
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COILED COIL (POTENTIAL).
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21.6%; Pred. No. 2.7;
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ACTIN-BINDING.
ACTIN-BINDING.
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InterPro; IPR000048; IQ.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              myosin_head; 1
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Pfam; PF000612; myosin_head; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF01276; Myosin_tail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYOSINHEAVY
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PIR, A02990, A02990.
PIR, A29320, A29320.
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Best Local Similarity 21.6
Matches 90; Conservative
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1915
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1120 IEELEEEIEAERTSRAKAEKHRADLSRELEEISERLEEAGGATAAQIDMNKKREAEFQKM 1179
                                                                                                 : |:|| : | | | |:| : | || 1339
1180 RRDLEEATLQHEATAAALRKKHADSTADVGEQIDNLQRVKQKLEKEKSELKMEIDDLASN 1239
                                                                                                                                                                            1296 VEEKDALISQLSRGKQAFTQQIEELKRHLEEEIKAKKCPAHALQSARHDCDLLREQYEEE 1355
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                                                                                                                                                                                                                                                                                                                                                                                                                               1416 CASLEKTKORLONEVEDLMIDVERSNAACAALDKKOKNFDKILSEWKOKYEETQAELEAS 1475
                                                                                                                                                      ----TIKANL-----IYADGKTQTAEFKGTFEEATAEAYRYADALKKDNGEYTVD 138
                                                                                                                                                                                                                                                                                                                                                                                          222 FAGKEKTPEEPKEEV-----TIKANLIYA--DGKTQT-----AEFKGTFAEATAE---- 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAPB_RAT STANDARD; PRT; 2459 AA.
P15205; 062958; Q9ER21; 09QW92;
01-APR-1990 (Rel. 14, Created)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
Microtubule-associated protein 1B (MAP 1B) (Neuraxin) [Contains: MAP1
                                                                                                                                                                                                                                     ----- EEPKEE 163
                                                                                                                                                                                                                                                                                                             164 VTIKANLIYADGK--TQTAEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIK 221
                                                                           92
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MEDLINE-90058971; PubMed=2555150;
Rienitz A., Grenningloh G., Hermans-Borgmeyer I., Kirsch J.,
Littauer U.Z., Prior P., Gundelfinger E.D., Schmitt B., Betz H.;
"Neuraxin, a novel putative structural protein of the rat central nervous system that is immunologically related to microtubule-
    -OTAEF---
                                                                           39 KGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             end of the rat microtubule-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-SPRAGUE-DAWLEY; TISSUE-Brain, and Glial tumor; MEDLINE-22347374; PubMed-1639022; Zaunter W., Kratz J., Staunton J., Feick P., Wiche G.; "Identification of two distinct microtubule binding dr recombinant rat MAP 1B.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INDUCTION
                                                                                                                                                                                                                                 139 VADKGYTLNIKFAGKE --------KTP----
  ------SEEEVTIKANLIFANGST-
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TRAIN-SPREAUE-DAWLEY, TISSUE-TESTIS;
MEDLINE-96257242; PubMed-8666295;
Liu D., Fischer I.;
alsolation and sequencing of the 5' end of associated protein (MAPIB)-encoding CDNA.'
Gene 172:307-308(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [4]
DEVELOPMENTAL STACE, AND PHOSPHORYLATION.
MEDLINE-97405699; PubMed=9260743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eur. J. Cell Biol. 57:66-74(1992).
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2 VENKEETPETPETD-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18;
Ma D., Nothias F., Boyne L.J., Fischer I.;
"Differential regulation of microtubule-associated protein 1B (MAPIB)
in rat CNS and PNS during development.";
J. Neurosci. Res. 49:319-32(1997)
-!- FUNCTION: The function of brain MAPS is essentially unknown.
Phosphorylated MAPIB may play a role in the cytoskeletal changes that accompany neurite extension. Possibly MAPIB Binds to at least two tubulin subunits in the polymer, and this bridging of subunits might be involved in nucleating microtubule polymerization and in
                                                                                                                                                                                                                               nerve levels are high early in development but decrease during postnatal development and are low in adults. In dorsal root ganglia levels remain high throughout development.

-!- DOMAIN: By nerve growth factor.

-!- DOMAIN: Has a highly basic region with many copies of the sequence KKEE and KKEI/V, repeated but not at fixed intervals, which is responsible for the binding of MAPIB to microtubules.

-!- PTM: LCl is coexpressed with MAPIB. It is a polypeptide generated from MAPIB by processing. It is free to associate with both MAPIA and MAPIB. It interacts with the amino-terminal region
                                                                                                                                                   can associate
                                                                                                                                                                                           cerebellum and cerebrum). Not expressed in liver, spleen, kidney,
                                                                                                                                                                                                                      DEVELOPMENTAL STAGE: In cerebral cortex, spinal cord and sciatic
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                                                                                                                                                                                                                                                                                                                                                                                           PTM: Phosphorylated.
SIMILARITY: TO MAPIA.
CAUTION: A C-terminal fragment of this protein (residues 1597 2459) was originally described as neuraxin in ref.3.
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                                                                                                                                 84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M -> V (IN REF. 1).
T -> S (IN REF. 1).
R -> K (IN REF. 3).
L -> I (IN REF. 3).
W; ZE3F6872DEDB8BA2 CRC64;
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MAP1 LIGHT CHAIN LC1.
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MAPIB 4.
MAPIB 5.
MAPIB 7.
MAPIB 9.
MAPIB 10.
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MAP1B 2.
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PROSITE; PS00230; MAP1B_NEURAXIN; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X60370; CAC16162.1; -. EMBL; X16623; CAA34620.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                  of MAP1B (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U52950; AAB17068.1; -.
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Matches 80; Conserv
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2169
2459
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1988
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CHAIN
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MIM; 157129;
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P14873;
                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                               Query Match
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REPEAT
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MAPB_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Microtubule-associated protein 1B (MAP 1B) [Contains: MAP1 light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENORICS 22:273-280(1994).

-!- FUNCTION: THE FUNCTION OF BRAIN MAPS IS ESSENTIALLY UNKNOWN.

-!- FUNCTION: THE FUNCTION OF BRAIN MAPS IS ESSENTIALLY UNKNOWN.

PHOSPHORYLATED MAPTE MAY PLAY A ROLE IN THE CYTOSKELETAL CHANGES

THAT ACCOMPANY NEURITE EXTENSION. POSSIBLY MAPIB BINDS TO AT LEAST

TWO TUBBLIN SUBBNITS IN THE POLYMER, AND THIS BRIGGING OF SUBNITS

MIGHT BE INVOLVED IN NUCLEATING MICROTUBULE POLYMERIZATION AND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STABILIZING MICROTUBULES.
SUBUNIT: 3 DIFFERENT LIGHT CHAINS, LC1, LC2 AND LC3, CAN ASSOCIATE WITH MAPIA AND MAPIB PROTEINS.
DOMAIN: Has a highly basic region with many copies of the sequence KKEE and KKELY, repeated but not at fixed intervals, which is responsible for the binding of MAPIB to microtubules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: LCI is coexpressed with MAPIB. It is a polypeptide generated from MAPIB by proteolytic processing. It is free to associate with both MAPIA and MAPIB. It interacts with the amino-terminal region
                        EEPSYTQDNDLSELISV--SQVEASPSTSSAHTPSQIASPLQE----DTLSDVVPPRDM 1750
                                                                       1807 TSSSPPIDAAAAEPYGFRSSMLFDTMQHHLALSRDLTTSSVEKDNGCKTPGDFNYAYQKP 1866
                                                                                                                                                                                                                                                            -EKTTKTPEDGGYSCEI----TEKTTRTPEEGGYSYEISEKT-----TRTPEVSGYT 1964
                                                       61 GEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIK-ANLIYADG------KTQTAEFK 111
                                                                                                                  --ALKKDNGEYTVDVADKGYT---LNIKFAGK 153
                                                                                                                                                                                                                                NGKYTVDVADKGYTLNIKFAGKEKTPEEPKE-----EVTIKANLIYADGKTQTAEFKGTF 258
EETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLK - - - - - KDN
                                                                                                                                                                         EKTPEEPKE-----EVTIKANLI--YADGKTQTAEFKGTFEEATAEAYRYADLLAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-95104835; PubMed-7806212; Jack L.M.; Reener C., Fischbach N., Kunkel L.M.; Caloning of human microtubule-associated protein 1B and the identification of a related gene on chromosome 15.";
                                                                                                                                                                                                                                                                                                                                                                                                  Ä
                                                                                                                                                                                                                                                                                                           259 AEATAEAYRYADLLAKENGKYTADLEDGGYTI 290
                                                                                                                 GT----FEEATAEAYRYAD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of MAP1B (By similarity). SIMILARITY: TO MAP1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L06237; AAA18904.1; -.
                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Fetal brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (
01-NOV-1995 (
16-OCT-2001 (
                                                                                                                                                                                                                                                                                                                                                                                               MAPB_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                             P46821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LC1].
MAP1B.
                                                                                                                                                                                                                                                                                                                                                                                 MAPB_HUMAN
                                                                                                               112
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PHOSPHORYLATED MAPIB MAY PLAY A ROLE IN THE CYTOSKELETAL CHANGES
THAT ACCOMPANY NEURITE EXTENSION. POSSIBLY MAPIB BINDS TO AT LEAST
TWO TUBULIN SUBUNITS IN THE POLYMER, AND THIS BRIDGING OF SUBUNITS
MIGHT BE INVOLVED IN NUCLEATING MICROTUBULE POLYMERIZATION AND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            610 ---КЕЕРЅРVКАЕVAEKQATDVKРКААКЕКТVККЕТКVКРЕDККЕЕКЕКРККЕVAKKEDK 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 TQ-TAEFKGTFEEATAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 VTIKANLIYADGKTQTAEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFA 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 713 VK-----KEEKKEVKKEEKEPKKEIKK----LPKDAKKSSTPLSEAKKPAALK-- 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 ENKEETPET-----PETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYA 53
                                                                                                                                                                                                                                                                                                                                                                                                   LYS-RICH (HIGHLY BASIC, CONTAINS MANY KKEE AND KKEI/V REPEATS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 motif unrelated to that of MAP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   560 ESKEETPEVTKVNHVEKPPKVESKEKVMVK-----KDKPVKTETKPSVTEKEVPS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 DTLKKDNGEYTVDVADKGYTLNIKFAGKEKT-----PEEPKEE-VTIKANLIYADGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domain of microtubule-associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1990 (Rel. 14, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Microtubule-associated protein 1B (MAP 1B) (MAP1.2) (MAP1(X))
[Contains: MAP1 light chain LCl].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 2468;
8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 125; DB 1; Length 246; Pred. No. 4.8; 40; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   540839CBDF09D461 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224 GKEKTPEEPKEEVTIKANLIYA-----DGKTQTAEFKGTFAEATAEA
                                                                                                                                  MAPIB 1.
MAPIB 2.
MAPIB 3.
MAPIB 4.
MAPIB 6.
MAPIB 6.
MAPIB 9.
MAPIB 9.
MAPIB 10.
                                                                                 Phosphorylation
TitterPro; IPR00102; MAP1B neuraxin.
Pfam: PF00414; MAP1B_neuraxin; 10.
PROSITE; PS00230; MAP1B_NEURAXIN; 6.
Microtubules; Repeat; Phosphorylatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-SWISS WEBSTER; TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAP1B contains a repeated sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell Biol. 109:3367-3376(1989)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1990 (Rel. 14, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAPIB OR MTAPIB OR MTAP5.
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                                                                                                                                                                                                                                                                                                                                            2047
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1946
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us-08-325-278b-1.rsp

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Streptococcus sp. (strain G148)
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P19909;
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                                                                                   Bacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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  DDT REPARED DD REPARED
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                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                            KKEE and KKEI/V, repeated but not at fixed intervals, which is responsible for the binding of MAPIB to microtubules. PTM: LCI IS COEXPRESSED WITH MAPIB. IT IS A POLYPEPTIDE GENERATED FROM MAPIB BY PROTECLYIC PROCESSING. IT IS FREE TO ASSOCIATE WITH BOTH MAPIB AND MAPIB. IT INTERACTS WITH THE AMINO-TERMINAL REGION
                 SUBUNIT: 3 DIFFERENT LIGHT CHAINS, LC1, LC2 AND LC3, CAN ASSOCIATE WITH MAPLA AND MAPLE PROTEINS.
                                                           DOMAIN: Has a highly basic region with many copies of the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---LNIKFAGKEKTPEEPKEEVTIKANLIY 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               699 KKETPLK-----DAKKEVKKEEKEVKKEEKEPKKEIKKISKDIKKSTPQSDTKKPSAL 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 KEEVTIKANLIYADGKTQT-AEFKGTFEEATAEAYRYADLLAKENGKYTVDV-ADKGYTL 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     560 ESKEETPEVTKTSQVEKTPKVESKEKVLVK-----KDKPVKTESKPSVTEKEVSS---- 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 ENKEETPE-----TPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONTAINS MANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        662 ------EDKT-----PLKKDEKPRKEEV-KKEIKKEIKKEEKKEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      219 NIKFAGKEK-TPEEPKEEVTIKANLIYADGKTQTAEFKGTFAEATAEA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FBD3DD99CFDBDA87 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAP1 LIGHT CHAIN LC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
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(Rel. 30, Last sequence update)
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MAPIB 4.
MAPIB 5.
MAPIB 6.
MAPIB 7.
MAPIB 8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:1306778; Mtaplb.
InterPro; IPR000102; MAPIB_neuraxin.
Pfam; PF00414; MAPIB_neuraxin; 10.
PROSITE; PS00230; MAPIB_NEURAXIN; 7.
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STABILIZING MICROTUBULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 DTLKKDNGEYTVDVADKGYT-
                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X51396; CAA35761.1;
                                                                                                                                                                                                           SIMILARITY: TO MAP1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71; Conservative
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1959
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1908
1925
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CHAIN
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P37575;
01-0CT-1994
01-0CT-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 DNGEYTVD-VADKGYTLNIKFAGKEKTPEEPK--EEVTIKANLIYADGKTQTAEFKGTFE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 DEDEFNWDSEEDKVF-----PV 108
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Immunoglobulin G binding protein G precursor (IGG binding protein G).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64
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; FBE12F83C7569A68 CRC64;
                                                                                                                                                                                                                                                                                                                                      Margolis P.S., Driks A., Losick R.;
Sporulation gene spoIIB from Bacillus subtilis.";
J. Bacteriol. 175:528-540(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.7%; Pred. NO. v...,
tive 41; Mismatches 125;
                                                                                                                         Firmicutes; Bacillus/Clostridium group;
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33.7%; Pred. No. 0.82;
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      Last annotation update)
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                                                                                                                                                         Bacillus/Staphylococcus group; Bacillus
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STRAIN=168 / PY79;
MEDLINE-93123172; PubMed=8419299;
16-OCT-2001 (Rel. 40, Last anno
Stage II sporulation protein B.
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122 G-
35923 MW;
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SubtiList; BG10912; spoIIB.
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Best Local Similarity 23...
To, Conservative
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                                                                                            Bacillus subtilis.
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Pseudomonas
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033479;
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                                                                                                                       Query Match
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                                                                                                                                                                                                            Filpula D., Alexander P., Fahnestock S.R.; "Nucleotide sequence of the protein G gene from Streptococcus GX7805, and comparison to previously reported sequences."; Nucleic Acids Res. 15:7210-7210(1987).
                                                                                                                                                                                                                                                                                                          MEDLINE=86300657; PubMed=3017704;
Guss B., Eliasson M., Olsson A., Uhlen M., Frej A.-K., Joernvall H.,
Flock J.-I., Lindberg M.;
"Structure of the IgG-binding regions of streptococcal protein G.";
EMBO J. 5:1567-1575(1986).
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLUIAR LOCATION: TYPE I membrane protein, Cell wall.
-!- SIMILARITY: TO OFHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS IN THE REGION OF THE MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMUNOGLOBULIN G BINDING PROTEIN G. EXTRACELLULAR (POTENTIAL).
MEMBRANE ANCHOR.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                             Malakauskas S.M., Mayo S.L.;
"Design, structure and stability of a hyperthermophilic protein
variant."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IgG-binding protein; Repeat; Transmembrane; Cell wall; Signal; 3D-structure.
                                                                                                                     Structure and evolution of the repetitive gene encoding
                                                                                            Olsson A., Eliasson M., Guss B., Nilsson B., Hellman U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALA-RICH.
3 X 37 AA REPEATS.
1-1.
1-2.
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EMBL; X00428; CAA68489.1; -
EMBL; X04015; CAA27638.1; -
PIR; S00128; S00128.
PIR; A26314; A26314.
PIR; A26314; A26314.
INTERPO; IPR0012988; GA.
INTERPO; IPR0012989; Gram_pos_anchor.
INTERPO; IPR001049; IGG_bind_B.
Pfam; PF001468; GA; 3.
Pfam; PF00746; Gram_pos_anchor; 1.
Pfam; PF00746; Gram_pos_anchor; 1.
PRINTS; PR00015; GPOSANCHOR.
PROSITE; PS00343; GRAM_POS_ANCHORING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Struct. Biol. 5:470-475(1998).
                                                                                                                                                Eur. J. Biochem. 168:319-324(1987)
                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-G148;
MEDLINE-98290449; PubMed-9628485;
                                                                 STRAIN=G148;
MEDLINE=88029445; PubMed=3665928;
                                                                                                                                                                                                 MEDLINE=88015586; PubMed=3658689;
                                                                                                                                                                                                                                                                                    SEQUENCE OF 114-593 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                            STRUCTURE BY NMR OF 371-427.
                                                                                                                                     streptococcal protein G
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593
567
588
593
111
111
290
215
                                                                                                          Lindberg M., Uhlen M.;
                                                     SEQUENCE FROM N.A.
                                                                                                                                                                         SEQUENCE FROM N.A.
                            NCBI_TaxID=1306;
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34
568
589
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104
179
                                                                                                                                                                                       STRAIN=GX7805
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                                                                                                                                                                                                                               18;
1-3.
2 X 55 AA REPEATS.
2-1.
2-2.
5 X 5 AA REPEATS OF [DE]-D-A-K-K.
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: MEMBRANE ENVIRONMENT OR AGGREGATION SEEMS TO BE REQUIRED FOR ICE NUCLEATION ACTIVITY.
-!- SUBCELLULAR LOCATION: Outer membrane (By similarity).
-!- DOMAIN: CONTAINS MANY IMPREPET REPEATS OF THE CONSENSUS OCTAPEPTIDE AGG-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
-!- SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN
                                                                                                                                                                                                                                                                                                                                                                             344 WIYDDATKTFTVTEKPEVIDASELTPAVTTYKLVI-----NGKT----LKG---ETTT 389
                                                                                                                                                                                                                                                                                                        299 PKTDTYK-----LILNGKT----LKG---ETTTEAVDAATAEKVFKQYANDNGVDGE 343
                                                                                                                                                                                                                                                                                                                                                     63 YTVDVADKGYTLNIK---FAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                       EAYRYADALK-----KDN---GEYTVDVADKGYTLNIK---FAGKEKTPEEPKEEVTIK 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168 ANLIYADGKTQTAEFKGTFEEATAEAYRYADLLAKEN---GKYTVDVADKGYTLN---IK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             501
                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                    12 PETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLK-----KDN---GE 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schmid D., Pridmore D., Capitani G., Battistutta R., Neeser J.-R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas syringae.";
FEBS Lett. 414:590-594(1997).
-!- FUNCTION: ICE NUCLEATION PROTEINS ENABLE BACTERIA TO NUCLEATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              390 EAVDAATAEKVFKQYANDNGVDGEWTYDDATKTFTVTEKPEVIDASELTPAVTTYKLVIN
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                                                                                                                                                                                                                               68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                      Score 122; DB 1; Length 593; Pred. No. 1.5;
                                                                                                                                                                                                                               87; Indels
                                                                                                                                             048BAA760D5B2920 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                               31; Mismatches
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                                                                                                                          PROTEINS
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                                                                                                                                             63291 MW;
                                                                                                                                                                                      7.8%; 27.9%;
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                                                                                                                                                                                                     Local Similarity
es 72; Conserv
                                                                                                                                             593 AA;
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254
303
303
373
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559
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FAMILY
    proteins.
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Lindow S.E., Lahue E., Govindarajan A.G., Panopoulos N.J., Gies D.;
"Localization of ice nucleation activity and the iceC gene product in
Pseudomonas syringae and Escherichia coli.";
Mol. Plant Microbe Interact. 2:262-272(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166
                                                                                                                                                                                                                                                                                                                                                                                                     SSLIAGYGSTOTAGFKSIMTAGYGSTQTAQERSDLVAGYGSTSTA-GYSSSLIAGYG--S 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 VDVADKGYTLNIKFAGKEKTPEEPKEEVT-----IKANLIYADGKTOTAEFKGTFE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 KANLIYADGKTQTAEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKE 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227 KTPEEPKEEVTIKANLIYADGKTQTAEFKGTFAE---ATAEAYRYADLLAKENGKYTADL 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         996
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                               64
                                                                                                                                                                                                                                                                                                                                                               ---TSEAYAYADTLKKDNGEYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               769 TQTAGYGSTLTTGY-GSTQTAQENSSLTTGYGSTSTAGYSSSLIAGYGSTQTAGYESTL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EATAEAYRYADALKKONGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVT-----I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        855 ASSLIAGYGSTQTAGY----ESTLTAGYGSTQTAQENSSLTTGY---GSTSTAGFASSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Green R.L., Warren G.J.;
"Physical and functional repetition in a bacterial ice nucleation
                                                                                                                                                                                                                                                                                                                  88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas syringae (pv. syringae).
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kajava A.V., Lindow S.E.; {\tt ^A} model of the three-dimensional structure of ice nucleation
                                                                                                                                                                                                                                                                     Length 1196;
                                                                                                                                                                                                                                                                                             ; Pred. No. 3.3;
33; Mismatches 110; Indels
                                                                                                                                                                                                   47 OCTAPEPTIDE PERIODICITY.
117991 MW; C9E9974CB1731E68 CRC64;
                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1200 AA.
                                                                                                                                                                                                                                                                                                                                                             24 ANLIFANGSTQTAEFK-----GTFEKA----
send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                     Score 122;
                                                                                                                                                    PROSITE; PS00314; ICE NUCLEATION; 42. Ice nucleation; Repeat; Outer membrane. DOMAIN 172 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                          Pfam; PF00818; Ice_nucleation; 61. PRINTS; PR00327; ICENUCLEATN.
                                     EMBL; AJ01086; CAA04521.1; -.
HSSP; P06620; 11NA.
InterPro; IPR000258; Ice_nucleatn.
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                                                                                                                                                                                                                                                                     7.8%;
                                                                                                                                                                                                                                         Query Match
Best Local Similarity 25.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 317:645-648(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                         SEQUENCE 1196 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                967 RSFLTAGY 974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MCBI_TaxID=321;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no we modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
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774 QTAGYESTLTAGYGSTQTAQENSSLTTGYGSTSTAGYSSSLIAGYGSTQTAGYESTL--- 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                716 SSLIAGYGSTQTAGFKSILTAGYGSTQTAQERTSLVAGYGST--STAGYSSSLIAGYGST 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 831 TA-----GSTQTAQERSDLVTGYGYAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 NLIYADGKTQTAEFKGTFEEATAEAXRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  861 SLIAGYGSTOTAGY----ESTLTAGYGSTOTAQENSSLTTGY---GSTSTAGFASSLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 PEEPKEEVTIKANLIYADGKTQTAEFKGTFAE---ATAEAYRYADLLAKENGKYTADLED
J. Mol. Biol. 232:709-717(1993)
-!- FUNCTION: ICE NUCLEATION PROTEINS ENABLE BACTERIA TO NUCLEATE CRYSTALLIZATION IN SUPERCOLED WATER.

CRYSTALLIZATION TO SUPERCOLED WATER.
                                                                                  -1- SUBCELLULAR LOCATION: OUTER membrane.
-1- DOMAIN: CONTAINS 122 IMPERFECT REPEATS OF THE CONSENSUS
OCTAPERTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A
REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
-1- MISCELLANEOUS: A STRUCTURAL MODEL IS SUGESTED IN WHICH THE .
NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1200;
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E3BEAD4BEA67ABB0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00818; Ice_nucleation, 61.
PRINTS; PR00327; ICENUCLEATN.
PROSTITE; PS00314; ICE_NUCLEATION; 40.
Ice nucleation; Repeat; Outer membrane; 3D-structure.
DOMAIN 176 1151 OCTAPEPTIDE PERIODICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Pred. No. 3.3; 33; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; DB 1;
3.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSP5_STRGN STANDARD; PRT; 1500 AA. P16952; 054184; 15.00-1990 (Rel. 15, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) Agglutinin receptor precursor (SSP-5). SSPB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.8%; Score 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR000258; Ice_nucleatn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1200 AA; 118587 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X03035; CAA26837.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 24.2
Matches 74; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDB; 1INA; 31-OCT-93.
PDB; 1INB; 31-OCT-93.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A24405; A24405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   978
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Conservative
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SIGNAL
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                                                                                                                                                                                                                                                                                                     -!- FUNCTION: MAY BIND STALIC ACID RESIDUES OF SALIVARY AGGLUTININ (SAG) IN A CALCIUAL DEPRENDENT REACTION. THE INTERACTION OF SAG WITH ITS RECEPTOR IN VARIOUS ORAL STREPTOCCCI MODULATE BACTERIAL COLONIZATION OF ORAL TISSUE AND IS ASSOCIATED WITH REDUCED LEVELS
                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Type I membrane protein. Cell wall.
DOMAIN: THE PRZ REGION, BY SIMILARITY WITH THE PROLINE RICH
MAD THE S.PYOGENES M6 PROTEIN AND STAPHYLOCOCCAL PROTEIN A,
HAY TRAVERSE THE CELL WALL PEPTIDOGLYCAN AND IS FOLLOWED BY
HYDROPHOBIC AA WHICH MAY FUNCTION TO ANCHOR THE PROTEIN TO THE
MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRO-RICH (PR2).
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                         Demuth D.R., Golub E.E., Malamud D.; "Streptococcal-host interactions. Structural and functional analysis of a Streptococcus sanguis receptor for a human salivary glycoprotein.";
                                                                                                                                                                                                                                             "Tandem genes encode cell-surface polypeptides SspA and SspB which mediate adhesion of the oral bacterium Streptococcus gordonii to human and bacterial receptors."; Mol. Microbiol. 20:403-413(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
CYTOPLASMIC (POTENTIAL).
TO M PROTEIN OF S.PYOGENES.
4 X APPROXIMATE TANDEM REPEATS, HR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPROXIMATE TANDEM REPEATS, PR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
W; DCF190E7D44D889F CRC64;
                                                                                                                                                                                                                 Demuth D.R., Duan Y., Brooks W., Holmes A.R., McNab R., Jenkinson H.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IN THE REGION OF THE MEMBRANE ANCHOR.
SIMILARITY: BELONGS TO THE SPAP/SSP5/SPAA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGLUTININ RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00746; Gram pos anchor; 1.
PROSITE; PS00343; GRAM_POS_ANCHORING; 1.
Signal; Repeat; Calcium-binding; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL. POTENTIAL.
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InterPro; IPR001899; Gram_pos_anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEINS
                                                                                                                                           Biol. Chem. 265:7120-7126(1990)
                                                                                                                                                                                                    MEDLINE-96310377; PubMed-8733238;
                                                                    MEDLINE=90236997; PubMed=2185241;
                                                                                                                                                                       REVISIONS, SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U40026; AAC44100.1; -.
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950
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                                      SEQUENCE FROM N.A.
Streptococcus.
NCBI_TaxID=1302;
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CA_BIND
SEQUENCE
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
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Length 1500;

DB 1;

Score 121.5; Pred. No. 4.5;

7.8%;

Query Match Best Local Similarity

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13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell wall; Transmembrane; Antibiotic resistance; Glycoprotein; Repeat;
                                                                           ETKDKGTATTATDNAQ----KQDEIKSDYAKQAEEIKTTTEAYKKEVAAHQAETDKINAE 169
                                                                                                                     YTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAY 122
                                                                                                                                                                                                                                                                                                                     271 EAIKORNETAKATY-EAAMKOYE-ADLAAIKKANEDNDADYQAKLAAYOTELARVOKANA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 X 2 AA TANDEM REPEATS OF D-[SAG].
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                         377
    Gaps
                                       ENKEETPETPETPEETSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=ISOLATE 1061;
Savolainen K., Kuusela P., Paulin L., Korhonen T.K.;
"Pls, a large repeat-rich surface protein of methicillin resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METHICILLIN-RESISTANT SURFACE PROTEIN.
                                                                                                                                                                                                                                                                                  ---KTQTAEFKGTFEEATAEAYRYADLLA--KENGKYTVDVADKGYTLNIKFAGKEKTPE
                                                                                                                                                                                                                                                                                                                                                                                          170 N--KAADDKYQKDL-----KSHQEEVEKI------NTANATAKAEYEAKLAQYQ
                                                                                                                                                                                                                                          211 KDLATVKKANEDSQQDYQNKLSAYQTELARVQKANAEAKEAYEKAVKENTAKNEALKVEN
                                                                                                                                                                                                                                                                                                                                                                 231 EPKE--EVTIKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKEN-----GKYTADL
                                                                                                                                                                                                    RYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKE--EVTIKANLIYADG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96270743; PubMed=8665912;
Hilden P., Savolainen K., Tyynelae J., Vuento M., Kuusela P.;
"Purification and characterisation of a plasmin-sensitive surface
protein of Staphylococcus aureus.";
Eur. J. Biochem. 236:904-910(1996).
  55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             676-682; 938-948; 1156-1168; 1176-1185;
Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75BE9ADB469BD309 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus."; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus.
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001899; Gram_pos_anchor.
Pfam; PF00746; Gram_pos_anchor; 1.
PROSITE; PS00343; GRAM_POS_ANCHORING; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P80544; Q92F62;
01-FBB-1996 (Rel. 33, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MRZ-2002 (Rel. 41, Last annotation update)
Methicillin-resistant surface protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus/Staphylococcus group; Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1637 AA; 174573 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF115379; AAD09131.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1199-1205 AND 1217-1224.
STRAIN-ISOLATE 1061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48
1637
1582
1603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 624-628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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InterPro; IPR001601; Meth-transf.
InterPro; IPR000051; SAM_bind.
SGD; S0005765; ABP140.
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                                                     12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PARTIAL SEQUENCE FROM N.A., SEQUENCE OF 1-12; 38-72; 102-115; 244-286; 560-574 AND 598-608, FUNCTION, AND SUBCELLULAR LOCATION.
                                                                                                            63 YTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAY 122
                                                                                                                                                                                                   134 -----TDKVETEEAPKAEETDKAT-----TEEAPKAEETDKATEEAP 170
                                                                                                                                                                                                                                                                                                                                                  218 EKTATEEAPKTEETDKVETEEAPK----AEETSKAATEKAPKAEETN----KVETEEA 267
                                                                                                                                                                                                                                     123 RYADALKKDNGEYTVDVADKGYTLNIKFA---GKEKTPEEPKEEVTIKANLIYA----D 174
                                                                                                                                                                                                                                                                         171 K-------TEETDKATTEEAPAAEETSKAATEEAPKAEETSKAATEEAPKAEET 217
                                                       Gaps
                                                                                       3 ENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Asakura T., Sasaki T., Nagano F., Satoh A., Obaishi H., Nishioka H., Imamura H., Hotta K., Tanaka K., Nakanishi H., Takai Y.; "Isolation and characterization of a novel actin filament-binding protein from Saccharomyces cerevisiae."; Oncogene 16:121-130(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLÜLAR LOCATION: Cytoplasm and cortical cytoskeleton. MISCELLANEOUS: A RIBOSOMAL FRAMESHIFT OCCURS BETWEEN THE CODONS
                                                                                                                                                                                                                                                                                                              175 GKTQTAEFKGTFEE---ATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  008641; 008644;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-MAR-2002 (Rel. 41, Last annotation update)
Actin-binding protein ABP140.
ABP140 OR YOR239W/YOR240W.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetaes; Saccharomycetaes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
STRAIN=S288C / FY1679;
MEDLINE=97127829; PubMed-8972580;
Boyer J., Michaux G., Fairhead C., Gaillon L., Dujon B.;
Roquence and analysis of a 26.9 kb fragment from chromosome XV c
"Sequence and analysis of cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Binds F-actin and shows weak F-actin crosslinking
                     Length 1637;
                                                                                                                                                                                                                                                                                                                                                                                      232 PKEEVTIKANLIYADGKTQTAEFKGTFAEATA----EAYRYADLLAKE 275
                                                                                                                                                                                                                                                                                                                                                                                                                         268 PAAEETNKA----ATEETPAVEDTNAKSNSNAQPSETERTQVVDTVAKD 312
         7.8%; SCOLE __ 27.3%; 27.3%; Pred. No. 4.9; **.ve 20; Mismatches 111; **.ve 20; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     627 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; 275147; CAA99460.1; ALT_SEO.
EMBL; 275147; CAA99461.1; ALT_SEO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98127445; PubMed=9467951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FOR LEU-276 AND GLY-277.
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BJ5457
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                   Query Match
Best Local S
Matches 799
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12;
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                                                                                                                                                                                                                                                                                                                                                                  63 YTVD---VADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKT------QTAEF 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 ESANNASEPAEEYSQSEEDADIE-----QSNGKETENAENASQQANDGSTSTTTSK 214
                                                                                                                                                                                4 NKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKK-DNGE 62
                                                                                                                                                                                                      171 IYADGKTQTA-EFKGTFEEATAEAYRYADLLAKENGKYTVDV-----ADKGYT----L
                                                                                                Length 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFAEATA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NKKKKNKKKKKKKKRNGNVNTNANV --- DDSTKTGENDDTTGDTTS 256
                                                           627 AA; 71354 MW; D4E55F9485412F39 CRC64;
52; Mismatches 103;
                                                                                                Score 121; DB 1;
Pred. No. 1.9;
                                                                                                7.7%; Score 121; 22.5%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: October 29, 2002, 09:29:54 Job time : 14.429 secs
                                                                                                                                         Conservative
                                                                                                                    Best Local Similarity
                                                                                                                                       64;
                                        INIT_MET
SEQUENCE
                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215
                                                                                                                                         Matches
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

October 29, 2002, 09:27:36; Search time 12.7943 Seconds (without alignments) 2290.646 Million cell updates/sec Run on:

US-08-325-278B-1 1565 1 AVENKEETPETPETDSEEEV......GGYTINIRFAGKKVDEKPEE 305 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum, DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

IES	Description	nid-ailodloonmmi	Iq light chain-bin	tein	iq light chain-bin	streptococcal surf	late embryogenesis	collagen adhesin -	late embryogenesis	late embryogenesis	NF-180 - sea lampr	embryonic protein	hypothetical prote	lactoferrin-bindin	130K surface exclu	fibrinogen-binding	choline binding pr	hypothetical prote	dextranase - Strep	internalin-like pr	surface exclusion	myosin heavy chain	neuraxin - rat	neurofilament prot	microtubule-associ	hypothetical prote	alpha-amylase (EC	F14L17.15 protein	mature-parasite-in	+
SUMMARIES	ΙD	A45063	A42808	554396	A34483	S42574	T47561	A42404	H84782	JC6171	151116	S04909	E72350	н81070	G41662	T28680	н98120	E89824	T30291	AF1772	S72375	A29320	S06017	T52485	A56577	T16588	A60990	C86278	A45605	637763
	DB	. 7	7	7	7	7	~	~	~	7	7	7	7	~	7	7	~	7	~	7	~	~	7	7	7	7	7	7	7	ç
	Length	455	719	992	74	664	479	1185	448	448	1110	555	992	737	891	1166	701	1141	1337	938	843	1940	863	913	2364	1035	955	673	~	463
ø	Query Match	100.0	99.7	78.4	11.0	10.7	10.6	6.7	9.6	9.5	9.0	9.0	8.8	8.5	8.4	8.4	8.3	8.3	8.3	8.3	8.1	8.1	8.1	8.1	8.1	8.1	8.1	8.0	8.0	α
	Score	1565	1561	1226.5	171.5	167	166	151.5	151	149	141.5	141	137.5	132.5	131.5	131.5	130.5	130.5	130.5	128.5	127.5	127.5	127	127	127	126.5	126	125.5	125.5	125
	Result No.		73	m	4	S	φ	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21		• 23	24	25	26	27	28	20

surface-located me	hypothetical prote	cyst germination s	ladder protein - C	microtubule-associ	hypothetical prote	EF protein - Strep	myosin heavy chain	surface exclusion	myosin heavy chain	probable peptidogl	endospore developm	hypothetical prote	protein G precurso	ice nucleation pro	probable cell surf
JC6009	D89808	T31108	T42223	QRMSP1	T39577	S33441	S52696	S22452	S24348	AF1450	C40646	G86287	800128	SNPSO	AD1525
٦	7	7	7	Т	7	7	7	7	7	7	7	7	7	Н	7
1302	495	1489	1198	2464	569	1822	698	890	955	1993	332	384	593	1200	657
8.0	7.9	7.9	7.9	7.9	7.9	7.9	7.8	7.8	7.8	7.8	7.8.	7.8	7.8	7.8	7.8
124.5	124	124	123.5	123.5	123	123	122.5	122.5	122.5	122.5	122	122	122	122	121.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 A45063 immunoglobulin-binding protein LG - Peptostreptococcus magnus C: Species: Peptostreptococcus magnus C: Species: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 15-Oct-1999 C; Accession: A45063 E; Kihlberg, B.M.: Sjobring, U.; Kastern, W.; Bjorck, L. J. Biol. Chem. 267, 25583-25588, 1992 A; Fitle: Protein LG: a hybrid molecule with unique immunoglobulin binding properties. A; Reference number: A45063; MUID:93094283 A; Accession: A45063 A; Status: preliminary A; Molecule type: mRNA; protein A; Residues: 1-455 < KIH> A; Molecule type: mRNA; protein A; Residues: 1-455 < KIH> A; Cross-references: GB:S50809; NID:g261705; PIDN:AAA03280.1; PID:g261706 A; Note: sequence extracted from NCBI backbone (NCBIN:120302, NCBIP:120303)	Ouery Match 100.0%; Score 1565; DB 2; Length 455; Best Local Similarity 100.0%; Pred. No. 2e-85; Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 AVENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSBAYAVADTLKKDN 60 	. GEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVIIKANLIYADGKTQTAEFKGTFEEATAE. 120 	. AYRVADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTA 180 	EFKGTFEBATAEAVRYADLLAKENGKYTUDVADKGYTLNIKFAGKEKTPEEPKEGVIKA 240 	NLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKVD 300 	EKPEE 305 EKPEE 326	A42808 19 light chain-binding protein precursor - Peptostreptococcus magnus N;Alternate names: protein L C;Species: Peptostreptococcus magnus C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999
A45063 Cimmunogial	Query Match Best Local Matches 30	Oy 1 Db 22	Qy 61 Db 82	Qy 121 Db 142	Oy 181 Db 202	Oy 241 Db 262	Qy 301 Db 322	RESULT 2 A42808 Ig light N;Alterna C;Species
								

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C;Accession: A34483
R;Akerstroem, B.; Bjoerck, L.
A;Tile: Protein L: an immunoglobulin light chain-binding bacterial protein. Characte A;Accession: A34483; MUID:90062074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Streptococcus dysgalactiae
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 19-May-2000
C;Accession: S42574
R;Jonsson, H.; Mueller, H.P.
Eur. J. Blochem. 220, 819-826, 1994
A;Title: The type-TII Fo receptor from Streptococcus dysgalactiae is also an alpha(2)
A;Reference number: S42574; MUID:94192673
A;Accession: S42574
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig light chain-binding protein L - Peptostreptococcus magnus (fragments) C;Species: Peptostreptococcus magnus C;Species: 07-Sep_1990 #sequence_revision 07-Sep-1990 #text_change 16-Aug-1996
                                         YRYADALKKDNGEYTVDVADKGYTLNIKFAGKE--KTPEEPKEEVTIKANLIYADGKTQT 179
                     EYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA 121
                                                                                                                                                                         180 AEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKE--KTPEEPKEEVT 237
                                                                                                                                                                                                                                                     238 IKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --TFEEATAEAYRYA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-664 <JON>
A;Cross-references: EMBL:229666; NID:9470220; PIDN:CAA82764.1; PID:9470221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVD 66
                                                                                                                                                                                               40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 664;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) DB 2;
J.00038;
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Pred. No. 0.000
5; Mismatches
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ilarity 58.2%;
Conservative
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A;Residues: 1-74 <AKE>
C;Keywords: immunoglobulin
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Best Local Similarity
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es 39; Conser
                                                                                                                                                                                                                                                                                                                              KVDEKPEE 305
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                                                         599
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                     62
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ب
                                                           repeated immu
                                                                                                           A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-719 <KAS>
A; Cross-references: GB:M86697
B; Kastern, W.; Holst, E.; Nielsen, E.; Sjoebring, U.; Bjoerck, L.
Infect. Immun. 58, 1217-1222, 1990
A; Title: Protein L, a bacterial immunoglobulin-binding protein and possible virulence A; Reference number: A41493; MUID:90215984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: S54396
R; Murphy, J.P.; Duggleby, C.J.; Atkinson, M.A.; Trowern, A.R.; Atkinson, T.; Goward, Mol. Microbiol. 12, 911-820, 1994
A; Title: The functional units of a peptostreptococcal protein L.
A; Reference number: S54396; MUID: 95020613
A; Accession: S54396
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A.Variety: strain 3316
C.Date: 27-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 15-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKAN 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: EMBL:L04466; NID:g150673; PIDN: AAA67503.1; PID:g150674
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                                                         οĘ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNG
             R; Kastern, W.; Sjoebring, U.; Bjoerck, L.
J. Biol. Chem. 267, 12820-12825, 1992
A; Tille: Structure of peptostreptococcal protein L and identification
A; Reference number: A42808; MUID:92316971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein L precursor - Peptostreptococcus magnus (strain 3316)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: DNA A;Residues: 1-992 <MUR>
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100.0%; Pred. No. 5.8e-85;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 78.4%
Best Local Similarity 79.9%
Matches 246; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  Query Match 99.7
Best Local Similarity 100.
Matches 304; Conservative
C; Accession: A42808; A41493
                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 202-275 <KA2>
C;Keywords: immunoglobulin
                                                                                             A; Accession: A42808
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C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 10-Nov-1995
C;Accession: A42404; S27665
C;Accession: A42404; S27665
J: Biol. Chem. 267, 4766-4772, 1992
A;Title: Molecular characterization and expression of a gene encoding a Staphylococcu
A;Reference number: A42404; MUID:92165839
A;Accession: A42404
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A;Residues: 1-448 <STO>
A;Cross-references: GB:AE002093; NID:94415909; PIDN:AAD20140.1; GSPDB:GN00139
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C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: H84782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      877 YIVEELTKVKGYTTHVDNNDMGNLIVTNKYTPETTSISGEKVWDDKDNQDGKRPEKVSVN 936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 937 LLANGEKVKTL------DVTSETNWKYEFKDLPKYDEGKKIEYTVTEDHVKDYTTDI-- 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --- EEVTIKANLIFANGSTQTAEFKGTFEKATS 47
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23.8%; Pred. No. 0.15;
tive 45; Mismatches 123;
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                                                                                        Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-1185 <PAT>
A;Cross-references: EMBL:M81736
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R. Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, Mayer, K.F.X.
Mayer, M.F.X.
Mayer, K.F.X.
Mayer, M.F.X.
Mayer, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   late embryogenesis abundant protein-like - Arabidopsis thaliana
N;Alternate names: protein F8J2.210
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000
                                                                                                                                                                        179
                                                                                                                                                                                                          67 VADKGYTLNIKFA---GKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAYR 123
                                                                                                                                                                                                                                                                                                                                                   437
                                                                                                                                                                                                                                                                                                                                                                                                             296
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DAPELTPALTTYKLVVKGN-TFSGETTTKAIDTATAEKEFKQ-YATANNV---DGEWSYD
                                                                                           381 KAIDAATAEKEFKQYATANGV---DGEWSYDDATKTFTVTEKPAVIDAPELTPALTTYKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                  -YADALKKDNGEYTVDVADKGYTLNIKFA---GKEKTPEEPKEEVTIKANLIYADGKTQT
                                                                                                                                                                                                                                                                                         AEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFA---GKEKTPEEPKEEV
                                                                                                                                                                                                                                                                                                                                                                                                          237 TIKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 166; DB 2; Length 47
Pred. No. 0.0072;
3; Mismatches 137; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43;
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25.8%;
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------MRLEGKKLDE 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: 3
A; Introns: 329/3; 382/2
A; Note: F8J2.210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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FTVTEKP 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82;
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Best Local S:
Matches 82,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               297
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C;Species: Petromyzon marinus (sea lamprey)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: 151116
R;Jacobs, A.J; Kamholz, J.; Selzer, M.E.
Brain Res. Mol. Brain Res. 29, 43-52, 1995
A;Title: The single lamprey neurofilament subunit (NF-180) lacks multiphosphorylation A;Reference number: 151116; MUID:95287814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 embryonic protein DC8 (clone 8/10) - carrot
C;Species: Daucus carota (carrot)
C;Date: 28-Peb-1990 #sequence_revision 28-Peb-1990 #text_change 21-Jul-2000
C;Accession: S04909
R;Franz, G.; Hatzopoulos, P.; Jones, T.J.; Krauss, M.; Sung, Z.R.
Mol. Gen. Genet. 218, 143-151, 1989
A;Fitle: Molecular and genetic analysis of an embryonic gene, DC 8, from Daucus carot
A;Reference number: S04909; MUID:89384429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
                                                             A;Residues: 1-1110 <JAC>
A;Cross-references: EMBL:U19361; NID:g632548; PIDN:AAA80106.1; PID:g632549
C;Superfamily: neurofilament triplet H protein
                              ---EPKEEV--TIKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLED 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NGEYTVDVADKGYT------LNIKFAGKEKTPEEPKEEVTIKANLIYADGKT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QTAEFKGTFEEATAEA-----YRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 PEE--PKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAYRYADLLAKENGKYTVDVADK 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 GYTLNIKFAGKEKTPEEPK------EEVTIKANLIYADGKTQTAEFKGTFAEATAE 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         685 ----VEAESKEEEEEDSKEADAEEDEAEEEEVKEEEVTKSDAEEAEAEAEEEAAKSEEE 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           482 SAEKDEEEEEEEKKEEEF-----AEAEEEEEDRGRKEGEAEAEEEEVEKEE 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  533 AEEAEVEEAEAEETEAEAAEEEEEAEGEEEAEAEGEEAEBEAEEVEEEAIE-----KA 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 639 EEEEAEEEEVTSK-----KAKTQEAE----VEEEEAEA---AEAEAEEEAEEEAGEED-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
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25.4%; Pred. No. 0.54;
live 38; Mismatches 138;
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A, Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                  : I | I |: |: |: 324
303 AGEVTROKMEEMRLEGKELKEE 324
                                                                                                                                   286 GGYTI-----NIRFAGKKVDEK 302
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Best Local Similarity 25.4*
Best Local Similarity 25.4*
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IS1116
NF-180 - sea lamprey
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C;Comment: This protein is a phosphotyrosine protein which belongs to late embryogenesis
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tate embryogenesis abundant protein - Arabidopsis thaliana
NyAlternate names: embryogenic cell protein 63; phosphotyrosine protein
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 21-Jul-2000
C; Accession: JC6171
R; Yang, H.; Saltou, T.; Komeda, Y.; Harada, H.; Kamada, H.
Gene 184, 83-88, 1997
A; Title: Arabidopsis thaliana ECP63 encoding a LEA protein is located in chromosome 4.
A; Reference number: JC6171; MUID:97169149
A; Accession: JC6171
A; Molecule type: mRNA
A; Residues: 1-448 cYAN>
                                                                                                                                                            14;
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                                                                                                                                                                                                                                                                 79 EAAESTKEGAQIASEKAVGAK------DATVEKAKET----ADYTAEKVGE 119
                                                                                                                                                                                                                                                                                                                      63 YTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAY 122
                                                                                                                                                                                                                                                                                                                                                        123 RYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEF 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 -----DYAVDKA-----VEAKDKTAEKAKETANYTADKA-KEAKDKTAEK 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | ::: | : | : | | 205 VGEYKDYTVDKAVEARDYTAEKATERAKDKTAEKTGEY-----KDYTVEKATEGKDVTVS 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259 KLGELKDSAVETAKRAMGFLSGKTREAKGKAVETKDT-----AKEN-----MEK 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79 EAAESTKEGAQIASEKAVGAK-----DATVEKAKET----ADYTAEKVGE 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 KGTFEEATAE-----AYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPE 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                            Gaps
                                                                                                                                                                                                               3 ENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 KGTFEEATAE-----AYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---EPKEEV--TIKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 RYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------DYAVDKA-----VEAKDKTAEKAKETSNYTADKA-KEAKDKTAEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.5%; Score 149; DB 2; Length 448; 24.5%; Pred. No. 0.067; tive 38; Mismatches 107; Indels
                                                                                                          Length 448;
                                                                                                    9.6%; Score 151; DB 2; Length 44
24.5%; Pred. No. 0.051;
Live 38; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       286 GGYTI ----NIRFAGKKVDEK 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            303 AGEVTROKMEEMRLEGKELKEE 324
                                                                                                 Query Match 9.6%
Best Local Similarity 24.5%
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 24.58
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 4, south part
C; Keywords: seed
           A;Gene: At2g36640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: AtECP63
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3
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Thu Oct 31 13:39:55-2002

<pre>Best Local Similarity 25.2%; Pred. No. 0.26; Matches 78; Conservative 30; Mismatches 130; Indels 72; Gaps 11; Qy 6 EETPETPSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAVADTLK 57</pre>	QY 247 GKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLED 285
	RESULT 13 H81070 Lactoferrin-binding protein B NMB1541 [imported] - Neisseria meningitidis (strain MC5 C;Species: Neisseria meningitidis C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
QY 117 ATAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKA 168 QY 117 ATAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKA 168 DD 277 KAKEYKEYAAQKAAEAKDATMGKTGEYKDYSAQKAAETKDATMEKTKE 324	C; Accession: H81070 R; Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. r.i, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Qy 169 NLIYADGKTQTAEFKGTFEBATAEAYRYADLLAKENGKYTVDVADKGY 216	A.Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoll, R.; A.Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A.Reference number: A81000; MUID:20175755 A.Accession: H81070
Qy 217 TLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKEN 276 1 1 1 1 1 1	A;Status: preliminary A;Molecule type: DNA A;Molecu
Qy 277 GKYTADLEDG 286 : Db 439 MEELKLQEEG 448	A;Tross_reletences; GB:AE0UZOU4; GB:AEDUZU96; NID:9/2Z0/83; FIDN:AAF41896.1; FID:9/2Z A;Experimental source: serogroup B, strain MC58 C;Genetics: A;Gene: NMB1541
	Query Match 8.5%; Score 132.5; DB 2; Length 737; Best Local Similarity 22.8%; Pred. No. 1.1; Matches 85; Conservative 50; Mismatches 137; Indels 101; Gaps 17;
.nytoure_transport in most of the included maritima (Strain Msbb) C:Species: Thermotoga maritima maritima C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000 C:Accession: E72350	QY 5 KEETPETPET-DSEEGVIK-ANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDN 60 :: :: :: :: :: :: : : : Db 81 KQDGTEIPDKHQAEEHLPLKEKDILFLDGTLKEQADKLKKKINERYSDVRVITSKKEE 138
<pre>Riversou, A.E.; Claycon, K.A.; Glil, S.K.; Gwinn, M.L.; Dodson, K.J.; Hatt, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M. Nature 399, 323-329, 1999</pre>	QY 61 GEYTUDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQT 107 Db 139 EKYQYQFVRAGYVFTRAEGKDNEKEKT-SDGKEFVNRFSYDGFVYYSGERPSQSLPSAGT 197
A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq. A. Reference number: A72200; MUID:99287316 A. Accession: E72360 A. Status: preliminary	QY 108 AEFKGTFE
A;Molecule type: DNA A;Residues: 1-992 <arn> A;Cross-references: GB:AE001738; GB:AE000512; NID:g4981158; PIDN:AAD35722.1; PID:g498116 A;Experimental source: strain MSB8</arn>	QY 139 VADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA 193
A,Gene: TM0638 Onerw Match 8 88. Grove 137 5. DB 2. Iength 002.	Qy 194YRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEV- 236 Dh. 316 DEPUT EDUTYANON EGGEEGMAGET AGNASVEGYDAGKARETERNANDER 372
Similarity 22.3%; Pred. No. 0.81; 7; Conservative 40; Mismatches 112;	237TIKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKE
QY 2 VENKEETPETDESEEVTIKANLIFANGSTQTAEFKGTFEKATS 47 : : : :	Db 373 PALSSGKHTKILDSLKISVDEASDKNPREFAISSMPDFGHPDKLLVEGREIPLVN 427 Qy 277 GKYTADLEDGGYT 289
QY 48 BAYAYADTLKKDNGEYTVDVADKGYTLNIKFAG 80 : :	Db 428 KEQTIELADGRKT 440
Qy 81 KEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAYRYAD 126 11	_ 5 (1)
Qy 127 ALKKDNGEYTUDVADKGYTLNIKFAGKEKTPEBPKEEVTIKANLIYADGKTQTAEFKGTF 186 1 :	C; Date: JU-Jun-1992 #sequence_revision JU-Jun-1992 #text_cnange is-Oct-1999 C; Ccession: G4166 G: Viksnins, A.S.; Gallo, J.C.; Dunny, G.M. R; Rao, S.M.; Olmsted, S.B.; Viksnins, A.S.; Gallo, J.C.; Dunny, G.M. J. Bacteriol. 173, 7650-7664, 1991
Qy 187 EEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYAD 246	A:Title: Molecular and genetic analysis of a region of plasmid pCF10 containing posit terococcus facelis. A:Reference number: A41662; MUID:92041679 A:Accession: G41662 A;Status: preliminary

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R;Josefsson, E.; McCrea, K.; Ni Eidhin, D.; O'Connell, D.; Cox, J.; Hook, M.; Foster, T Microbiology 14, 3387-3395, 1998
M;Crobiology 14, 3387-3395, 1998
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M;Crobiology 14, 387-3395, 1998
M;Crobiology 15, 126880
A;Reference number: 220510; MUID:99098700
A;Reference number: 220510; MUID:99098700
A;Reference number: 220510; MUID:99098700
A;Reference number: 200510; M
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                                                                                                                                                                                                                                                                                                                                     11;
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89 QSVKDQQAVVD----QNKDALDQSQQAVT-----DQQAVVDEAKKVVDEATPSAIEK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 A-----DALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 TAEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTI 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | : || :| |: i || || || 241 KDDQAVADQQTVVTTSQEKVTDAKADTAA-KQADLTAKENALKDKQAATKQAQNTLDNSK 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 -DKGYTLNIKFAGKEKTPEEPKEEVTI------KANLIY------ 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             474 DDYG---NIKL-GNGSTIIDQNTEIKVYKVNSDQQLPQSNRIYDFSQYEDVTSQFDNKKS 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----ADGKTQTAEFKGTFEEATAEAYRYADALKKDN 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----GEYTVDVADKGYTL----NIKFAGKEKTPEEPKEEVTIKANLIYADGK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 KANLIYADGKT--QTAEFKGTFAEATAEAYRYADLLAKENG----------------277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 VDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAYRY 124
                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                     5 KEETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYT 64
A;Molecule type: DNA
A;Residues: 1-891 <KAO>
A;Csoss-references: GB:M64978; NID:g150552; PIDN:AAA65847.1; PID:g150554
C;Genetics: A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 EQAOPKTPENSSTEOPTVKATQTTEQAITEKQQQVTEKQAIVDQKQQVADTAKKEKDAID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188 QAVTAAKQEQAKLEE-----LAKNAEAEKVKAEKEQAAKEAELANKQKEEAKAKDQKT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---KYTAD-----LEDGGYTINIRFAGKKVDEKPEE 305
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                                                                                                                                                                                                                                                8.4%; Score 131.5; DB 2;
22.1%; Pred. No. 1.6;
tive 46; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 8.4%; Score 131.5; DB 2; Best Local Similarity 20.4%; Pred. No. 2.2; Matches 82; Conservative 46; Mismatches 134;
                                                                                                                                                                                                                                                                                           Best_Local Similarity 22.1%
Matches 78; Conservative
                                                                                                                                                                                                                                                         Query Match
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October 29, 2002, 09:28:27; Search time 9.49256 Seconds (without alignments) 784.805 Million cell updates/sec
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1 AVENKEETPETPETDSEEEV......GGYTINIRFAGKKVDEKPEE 305
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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3: /cgn2_6/ptcdata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:*

Database :

	Description	Sequence 1, Appli	Sequence 3, Appli	7	4	9	9	13,	13,	8, A	æ	4,	4	7	7	æ	9	Sequence 7, Appli	Sequence 5, Appli	Sequence 2, Appli	2,	9	25,	2, 4		Sequence 118, App	Sequence 4, Appli	4
SUMMARIES	D C	US-08-795-475-1	US-08-795-475-3 (US-08-446-137B-2	US-08-446-137B-4	US-08-828-741B-6	US-09-160-567-6	US-08-828-741B-13	US-09-160-567-13	US-08-828-741B-8	US-09-160-567-8	US-08-828-741B-4	US-09-160-567-4	US-08-828-741B-2	US-09-160-567-2	US-08-446-137B-8	US-08-446-137B-6	US-08-446-137B-7	US-08-446-137B-5	US-08-669-408B-2	US-08-447-031A-2	US-09-308-022-6	US-08-847-065-25	PCT-US93-05944-2	US-08-961-083-120	US-08-961-083-118	US-08-409-995-4	US-08-685-467-4
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, مه	Ouery Match	100.0	100.0	78.4	7.77	39.5	39.2	39.3	39.3	39.3	39.3	39.2	39.2	39.2	39.5	21.3	20.2	19.6	19.4	10.7	6.7	8.2	8.1	7.9	7.8	7.8	7.4	7.4
	Score	1565	1565	1226.5	1216	618	618	615	615	615	615	614	614	613	613	334	315.5	306	303	167	151.5	128.5	127.5	123	121.5	121.5	116.5	116.5
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Gaps

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Length 305; Indels

Query Match 100.0%; Score 1565; DB 2; Best Local Similarity 100.0%; Pred. No. 1.6e-126; Matches 305; Conservative 0; Mismatches 0;

1 AVENKEETPETPETDSEEEVIIKANLIFANGSTQTAEFKGTFEKATSEAXAYADTLKKDN 60

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Sequence 33, Appli Sequence 4, Appli Sequence 47, Appl Sequence 28, Appli Sequence 34, Appli Sequence 4, Appli Sequence 1, Appli Sequence 1, Appli Sequence 156, Appli		THEREOF
28 116.5 7.4 2353 4 US-09-377-155-33 29 116.5 7.4 2353 4 US-08-913-942-4 33 31 116.5 7.4 2353 4 US-08-913-942-4 33 32 116.5 7.4 2354 4 US-09-268-347-47 34 115. 7.4 1104 4 US-09-268-347-24 35 116 7.4 1104 4 US-09-268-347-34 35 115 7.3 272 2 US-08-193-159-4 36 115 7.3 272 2 US-08-193-159-4 36 115 7.3 337 2 US-08-193-159-8 39 115 7.3 337 3 US-08-193-156-8 40 115 7.3 365 4 US-08-897-438-156 41 115 7.3 404 4 US-08-897-438-156 42 115 7.3 411 4 US-08-897-438-154 43 115 7.3 411 4 US-08-897-438-154 45 115 7.3 417 3 US-08-897-438-155 43 115 7.3 411 3 US-08-897-438-155 43 115 7.3 411 3 US-08-897-438-155 44 115 7.3 411 3 US-08-897-438-153	ALIGNMENTS	ESULT 1 US-08-795-475-1 US-08-795-475-1 Sequence 1, Application US/08795475 Patent No. 5965390 GENERAL INFORMATION: APPLICANT: SJVDTING, U1f TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS NUMBER OF SEQUENCES: 14 TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS NUMBER OF SEQUENCES: 14 TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS CORRESPONDENCE SEED and BERRY LLP STREET: 6300 Columbia Center, 701 Fifth Avenue CITY: Seattle STREET: Washington COUNTRY: USA 21P: 98104-7092 COMPUTER: Has PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: 11-FEB-1997 CLASSIFICATION NUMBER: US/08/795,475 FILING DATE: 11-FEB-1997 CLASSIFICATION NUMBER: 13,963 ATTORNEY AGENT INFORMATION: REFIERNOE/DOCKET NUMBER: 100084.402D1 TELEPHONE: (206) 682-6031 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH 305 amino acids TYPE: amino acids TYPE: MICHORY HYPOTHETICAL: NO ORGANISM: Escherichia coli LE392/PHDL, DSM 7054

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EFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKA 240
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APPLICANT: Trowern, Angus R.
APPLICANT: Atkinson, Anthony
APPLICANT: Murphy, Jonathan P.
APPLICANT: Laurence, Oliver S.
APPLICANT: Laurence, Oliver S.
APPLICANT: Duggleby, Clive J.
TITLE OF INVENTION: IMMUNGLOBULIN BINDING PROTEINS DERIVED
TITLE OF INVENTION: FROM L PROTEIN AND THEIR USES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0, Version #1.30
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79.9%; Pred. No. 7.7e-97
tive 22; Mismatches 3
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CLASSIFTCATION: 514
ATTORNEY AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33-963
REFERENCE/DOCKET NUMBER: 100084.406
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,137B
FILING DATE: 22-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08446137B Patent No. 6162903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-631
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 79.9%
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MEDIUM TYPE: Floppy
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Washington
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                                                                                                              AYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Bjvrck, Lars
APPLICANT: Sjvbring, Ulf
APPLICANT: Sjvbring, Ulf
APPLICANT: Sprbring, Ulf
CORRESPONDENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/795,475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 100.0%; Score 1565; DB 2; Best Local Similarity 100.0%; Pred. No. 2.7e-126; Matches 305; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08795475 Patent No. 5965390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCMSters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 1000:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-631
INPORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
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CITY: Seattle
STATE: Washington
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EKPEE 305
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EATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKE--KTPEEPKEEVTIKANLIYA 245
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                                    KGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAYRYADALK 129
                                                                                                         KDNGEYTVDVADKGYTLNIKFAGKE--KTPEEPKEEVTIKANLIYADGKTQTAEFKGTFE 187
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 2 ETPE--PEEEVTIKANLIFADGSTQNAEFKGTFAKAVSDAYAYADALKKDNGEYTVDVAD
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                                                                                                                                                                                                                                                DGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGK 297
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                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 14
ANDRESSER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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ZIP: 11530

MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,741B
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Pred. No. 1.9e-45;
5; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: SCULLY, SCOTT, MURPHY & PRESSER 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ...muc DATE: 26-MAR-1997
CLASSIFICATION: 435
TORNEY/AGENT ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      United States of America
                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08828741B Patent No. 6043069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31.346
REFERENCE DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 6:
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75.9%;
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Best Local Similarity 75.9
Matches 126; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-828-741B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Garden City
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APPLICANT: Koentg
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                                                                                                                                                                                                                                                                  276 MERKLSEKETPE--PEEEVTIKANLIFADGSTQNAEFKGTFAKAVSDAYAYADALKKDNG 333
                                                                                                       YRYADALKKDNGEYTVDVADKGYTLNIKFAGKE--KTPEEPKEEVTIKANLIYADGKTQT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETPETDSEEEVTIKANLIFANGSTQTAEFKGTFERATSEAYAYADTLKKDNGEYTVDVAD 69
                                                                                                                                                                           AEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKE--KTPEEPKEEVT
                                                                                                                                                                                                                                             238 IKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Atkinson, Anthony
APPLICANT: Murphy, Jonathan P.
APPLICANT: Murphy, Jonathan P.
APPLICANT: Laurence, Oliver S.
APPLICANT: Duggleby, Clive J.
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEINS DERIVED
TITLE OF INVENTION: FROM L PROTEIN AND THEIR USES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 291;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,137B
FILING DATE: 22-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77.7%; Score 1216; DB 4;
82.5%; Pred. No. 1.1e-96;
tive 20; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 100084.406
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08446137B Patent No. 6162903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Trowern, Angus R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Seattle
STATE: Washington
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CLASSIFICATION:
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---EQPGE 578
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Sequence 13, Application US/08828741B
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US-09-160-567-13
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234 IKFAGKEATNRNTDGSTDYGILQINSRWGGLTSAEEVTIKANLIFANGSTQTAEFKGTFE 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20; Gaps
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Pred. No. 1.9e-45;
5; Mismatches 15; Indels
                                                                                                                                                                                                                                                 APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CAPALYTIC ANTIBODIES AND A METHOD OF
                                       Oy - 116 EATAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPR 161

Db 294 KATSEXYAADTLKKDNGEYTVDVADKGYTLNIKFAGKESANRHPQ 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        294 KATSEAYAYADTLKKDNGEYTVDVADKGYTLNIKFAGKESAWRHPQ 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPETWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/160,567
                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STRIE: 400 Garden City Plaza
CITY: Garden City
STATE: New York
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FILLING DATE:
FILLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DiGIGIO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEFAX: (516) 742-4343
TELEFAX: (516) 742-4366
TELEFAX: 230 901 SANS UR
FILEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 6:
SEGUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New York
COUNTRY: United States of America
ZIP: 11530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,741
                                                                                                                                                                                       Sequence 6, Application US/09160567
Patent No. 6326179
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75.9%;
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amino acid
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Best Local Similarity 75.9
Matches 126; Conservative
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                                                                                                                                                RESULT 6
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US-08-828-741B-13

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 615; DB 3; Length 178;
Pred. No. 1.4e-45;
5; Mismatches 14; Indels
                                           APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13, Application US/09160567

Patent No. 6326179

GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: TreutLian, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 TAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPK 161
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PACAMIN PC-DOS/MS-DOS
SOFTWARE: PACAMIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                               SEE: SCULLY, SCOTT, MURPHY & PRESSER: 400 Garden City Plaza Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 1059
TELECOMMUNICATION INFORMATION:
TELEFAX: (516) 742-4343
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 13:
                         Koentgen, Frank
Suess, Gabriele M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39.3%;
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NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
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Best Local Similarity 76.2
Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-828-741B-13
                                                                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
FILING DATE: 26-MAR
CLASSIFICATION: 435
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GENERAL INFORMATION:
APPLICANT: Koento
                                                                                                                                                                                                                                                                   STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 39.3%; Score 615; DB 3; Length 198; Best Local Similarity 76.2%; Pred. No. 1.6e-45; Matches 125; Conservative 5; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
APPLICANT: Stoesk Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: PRODUCING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 TAEAYRYADALKKONGEYTVDVADKGYTLNIKFAGKEKTPEEPK 161
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,567
      PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: A00 Garden City Plaza CITY: Garden City Plaza STATE: New York
SOFTWARE: Patentin Netters Current Paper State S
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NAME: DiGigilo, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/09160567
Patent No. 6326179
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-828-7418-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 FAGKEKTPEE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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US-09-160-567-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 EEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLNIK 77
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Patent No. 6043069

GENERAL INPORMATION:
APPLICANT: Koentgen, Frank
APPLICANT: Tarlinton, David M.
APPLICANT: Treuliein, Herbert R.
TITLE OF INVENTION: CAPALYIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 615; DB 4; Length 178;
Pred. No. 1.4e-45;
5; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 TAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPK 161
                                                                                                           ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEE: SCULLY, SCOTT, MURPHY & PRESSER: 400 Garden City Plaza Garden City
                                                                                        United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                United States of America
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DiG191LO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEFRAX: (516) 742-4346
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 13:
400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.3%;
76.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 178 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 76.2
Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-09-160-567-13
                              Garden City
New York
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                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 11530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-828-741B-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                             STATE:
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Garden City
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Matches 125; Conser
                 Similarity
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                                                                                                                                                76 IKFAGKEKTPEE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 11530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                   Best Local Sin
Matches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-160-567-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                             92 FACKEATURNTDGSTDYGILQINSRWGGLTSAEEVTIKANLIFANGSTQTAEFKGTFEKA 151
                                                                                                                                                                                                                                                              20; Gaps
                                                                                                                                                                                                                                                                                                 18 EEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLNIK 77
                                                                                                                                                                                                                                                                                                                     32 EEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLIIK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INCORNATION:
APPLICANT: Suess, Gabriele M.
APPLICANT: Suess, Gabriele M.
APPLICANT: Treutlin, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF TITLE OF INVENTION: PRODUCING SAME NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER STRET: ADO Garden City Plaza CITY: Garden City Plaza
STATE: New York
                                                                                                                                                                                                                          Length 198;
                                                                                                                                                                                                                                                              14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 TAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTOTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DAPR:
APPLICATION NUMBER: US/08/828,741B
FILING DATE: 26 MAR-1997
                                                                                                                                                                                                                        Score 615; DB 4;
Pred. No. 1.6e-45;
                                                                                                                                                                                                                                             Pred. No. 1.6e
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08828741B Patent No. 6043069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DiG1911O, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 1059:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELES: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
               TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELES: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                          39.3%;
76.2%;
                                                                                                            : 198 amino acids
amino acid
                                                                                                                                                                                                                    Query Match 39.3
Best Local Similarity 76.2
Matches 125; Conservative
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                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-160-567-8
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US-08-828-741B-4
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                                                                                                            LENGTH:
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                                                                                                                                                                                     -PKEEVTIKANLIYADGKTQTAEFKGTFE 115
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                                                                                                                    |||||||| |
234 IKFAGKEATNRNTDGSTDYGILQINSRWGGLTSAEEVTIKANLIFANGSTQTAEFKGTFE 293
                                                                                          16 SEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLN 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 SEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLN 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20;
                                                20;
Score 614; DB 3; Length 495;
Pred. No. 6.8e-45;
1; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                     294 KATSEAYAYADTLKKDNGEYTVDVADKGYTLNIKFAGKE 332
                                                                                                                                                                                                                                                                            116 EATAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKE 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 614; DB 4;
Pred. No. 6.8e-45;
1; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/160,56' FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08/828,741
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09160567
Patent No. 6326179
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
  39.2%;
78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39.2%;
78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SAS UR
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 495 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 IKFAGKEKTPEE-----
                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
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GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 613; DB 3; Length 182
Pred. No. 2.1e-45;
5; Mismatches 9; Indels
                                                                                                                                                                                                                            APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Tralinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CAPALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 11530
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,741B
FILING DATE: 26-MAR-1997
CLASSIFICATION: 435
                                                                    294 KATSEAYAYADTLKKDNGEYTVDVADKGYTLNIKFAGKE 332
                                                     EATAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKE 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 EEATAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAG 152
                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                            New York : United States of America
                                                                                                                                                                         Sequence 2, Application US/08828741B Patent No. 6043069 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: DIGGGILO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4346
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 182 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Séquence 2, Application US/09160567
Patent No. 6326179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.2%;
78.5%;
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Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                         Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                          RESULT 13
US-08-828-741B-2
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CITY: Ga
                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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------KEEVTIKANLIYADGKTQTAEFKGTF 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Trowern, Angus R.
APPLICANT: Atkinson, Anthony
APPLICANT: Murphy, Jonathan P.
APPLICANT: Laurence, Oliver S.
APPLICANT: Dugdleby, Clive J.
APPLICANT: IMMUNOSLOBULIN BINDING PROTEINS DERIVED TITLE OF INVENTION: FROM L PROTEIN AND THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.2%; Score 613; DB 4; Length 182; 78.5%; Pred. No. 2.1e-45; Live 5; Mismatches 9; Indels
                  APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                   Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 EEATAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: SCULLY, SCOTT, MURPHY & PRESSER 400 Garden City Plaza
                                                                                                                                                                                                                                                New York
United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-436
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,567
                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-446-137B-8
; Sequence 8, Application US/08446137B
; Patent No. 6162903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 NIKFAGKEKTPEEP------
  Koentgen, Frank
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amino acid
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Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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                                                                                                                                                                                                 STREET: 400 Garder
CITY: Garden City
STATE: New York
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                                                                                                                                                                                                                                                                COUNTRY: Un
ZIP: 11530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
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APPLICANT:
APPLICANT:
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1;

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Length 75;
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MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC compatible
COMPUTER: PARTINE COMPUTER: PLORENT FOLDOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,137B
FILING DATE: 22-MAY 1995
CLASSIFICATION: 514
ATTONEY/AGENT INFORMATION:
NAME: MCMASTERS, DAVID D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 100084.406
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NOT: 8:
TELECOMMUNICATION OF: 8:
TELECOMMUNICATION OF: 8:
TELECOMMUNICATION OF: 8:
TELECOMMUNICATION OF: 8:
TELECOMMUNICATION SEQID NOT: 8:
TELECOMMUNICATION SEQUENCE: TELECOMMUNICATION SEGUENCE
TELECOMMUNICATION SEGUENCE: TELECOMMUNICATION SEGUENCE
TELECOMMUNICATION SEGUEN
                                           ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 334; DB 4;
Pred. No. 4.5e-22;
4; Mismatches 3
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Best Local Similarity 90.1%;
Matches 64; Conservative
CORRESPONDENCE ADDRESS:
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0;

0; Gaps

3; Indels

287 GYTINIRFAGK 297

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Search completed: October 29, 2002, 09:31:54 Job time: 11.4926 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

October 29, 2002, 09:25:06 ; Search time 23.9378 Seconds (without alignments) 1415.233 Million cell updates/sec Run on:

Title:

US-08-325-278B-1 1565 1 AVENKEETPETPETDSEEEV.......GGYIINIRFAGKKVDEKPEE 305 Perfect score:

Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

747574 seqs, 111073796 residues

Searched:

Total number of hits satisfying chosen parameters:

747574

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

1: SIDS1/gcgdata/geneseq/geneseqp-emb1/Aa1980.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS1/gcgdata/geneseg/genesegp-emb1/AA2000.DAT:*/SIDS1/gcgdata/geneseg/genesegp-emb1/AA2001.DAT:*

			Description	Immunoglobulin lig	Sequence encoding	Amino acid sequenc	Expression vector	Protein L. Peptoc	Protein L. Peptoc	Immunoglobulin bin	Growth factor TLHL	TLHL amino acid se	Growth factor LHL-	Amino acid sequenc
ES	~	Ś	7		9	1 Table 10 T	ğ							
SUMMARIES			\ q ₁		AAR42994	AAB31372~	AAB10432	AAR42203	AAR43699	AAR42204	AAW32482	AAY06909	AAW32486	AAY06913
			DB	14	14	22	21	14	14	14	18	20	18	20
			Length	305	434	467	367	1027	1027	291	342	342	178	178
	æ	Query	Match Length DB 1	100.0	100.0	98.7	87.3	78.4	78.4	77.7	39.5	39.5	39.3	39.3
			Score	1565	1565	1544.5	1366	1226.5	1226.5	1216	618	618	615	615
		Result	No.	1	7	ю	4		9	7	80	6	10	11

	Growth factor CATA	CATAB-TEV aminoaci Growth factor LHL	LHL growth factor	Amino acid sequenc	Peptostreptococcus	Peptostreptococcus	Peptostreptococcus	Peptostreptococcus	Ig light chain bin	Peptostreptococcus	PpL mutant protein		nutant	nutant	strept	Peptostreptococcus	Peptostreptococcus	S. dysgalactiae MI	Collagen binding p	A. thaliana enviro	Enterococcus faeca	Enterococcus faeca	Enterococcus faeca	Amino acid sequenc	S. aureus SdrE pro	N-terminal truncat	Choline binding pr	N-terminal region	N-terminal choline	no acid	C3 binding protein
AAW32481 AAY06910	AAW32480	AAK 100908 AAW 32479		AAY06915	AAY82537	AAY82538	AAY82540	AAY82539	AAY82536	AAY82544	AAY82545	AAY82548	AAY82546	AAY82547	AAY82542	AAY82543	AAY82541	AAR71929	AAR22675	AAY77965	AAY00138	AAY00140	AAY00142	AAY49150	AAY08643	AAY49231	AAY32103	AAY49247	AAY32186	AAY49144	AAW62654
18 20	18	18	20	20	21	21	21	21	21	21	21	21	21	21	21	21	21	16	13	21	20	20	20	20	20	20	20	20	20	20	19
198 198	495	182	182	482	9/	72	72	72	82	75	82	82	82	82	71	74	71	664	1185	448	1638	1638	1638	414	1166	376	376	413	413	414	564
	•	39.2					23.6								20.3	19.6	19.4					9.0			8.4	•	8.3				٠
615 615	614	613	613	809	389	371	370	369	341	334	334	334	332	328	315.5	306	303	167	154.5	149	141.5	141.5	141.5	131.5	131.5	130.5	130.5			。	130.5
12 13	14	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

AAR42993 standard; Protein; 305 AA. (first entry) 16-MAY-199 AR42993 RESULT 1 AAR42993

Immunoglobulin light chain binding protein (Protein L).

Immunoglobulin; light chain; binding; identification; purification; separation.

E. coli LE392/PHDL, DSM 7054.

5..305 /label= B1 immunoglobulin light chain binding 81..305 /label- B2 immunoglobulin light chain binding Location/Qualifiers domain. Domain Domain Key

/label= B3 immunoglobulin light chain binding /label= B4 immunoglobulin light chain binding domain. domain. 225..305 153..305 Domain Domain

/label= B5 immunoglobulin light chain binding domain. 297..305

domain.

Jomain

WO9322342-A

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/label= Bl immunoglobulin light chain binding
                                                                                                                                                                                                                                                                    /label= C2 immunoglobulin heavy chain binding
                                                              /label= B2 immunoglobulin light chain binding
                                                                                                /label= B3 immunoglobulin light chain binding
                                                                                                                               /label- B4 immunoglobulin light chain binding
                                                                                                                                                                  /label= B5 immunoglobulin light chain binding
                                                                                                                                                                                                  /label= C1 immunoglobulin heavy chain binding
                                                                                                                                                                                                                                   /label= D intermediate immunoglobulin heavy
                                                                                                                                                                                                                                               chain binding domain
        Location/Qualifiers
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                                                                                                             domain.
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Best Local Similarity 100.
Matches 305; Conservative
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P-PSDB; AAR42994.
                                                                                                                                                       297
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                                                                                                                                                                                                                                                                                                                                                   28-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                        28-APR-1992;
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          Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKVD 300
                                                                                                                                                                                                                      light chains. It is useful for binding, separating (purifying) and identifying immunoglobulin and for removing immunoglobulin molecules from serum. Hybrid proteins of the L protein can bind all human immunoglobulin classes and many immunoglobulins from other species. They are highly soluble and retain their binding activity at high without loss over a pH range of 3-10. They can be immobilised without loss of activity.
                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                   1 AVENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin; light chain; binding; identification; purification;
                                                                                                                                                                                                                                                                                                                                                                                             1 AVENKEETPETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYADTLKKDN
                                                                                                                                                                                                             protein (Protein L) is capable of binding to immunoglobulin G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKA
                                                                                                                                           protein L binding light chains of all immunoglobulin classes
                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                      DB 14; Length 305;
                                                                                                                                                     - for binding purifying and identifying immunoglobulin, also related DNA, vectors and host cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence encoding immunoglobulin light chain binding protein.
                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                      Score 1565; DB 14;
Pred. No. 2.2e-110;
                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR42994 standard; Protein; 434 AA.
                                                                                                                                                                                       Claim 1; Page 36; 71pp; English.
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0
                                                                                                                                                                                                                                                                                                                                      100.0%;
100.0%;
                                                              (HIGH-) HIGHTECH RECEPTOR AB
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                                       92SE-0001331.
                   93WO-SE00375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 305; Conservative
                                                                                   Sjoebring
                                                                                                        WPI; 1993-368722/46.
N-PSDB; AAQ50452.
                                                                                                                                                                                                                                                                                                                305 AA;
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EKPEE 305
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                  28-APR-1993;
                                      28-APR-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            separation;
                                                                                    Bjoerck L,
                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                      Query Match
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61 GEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAE 120 121 AYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTA 180 Protein L (AAR42993) is capable of binding to immunoglobulin G light chains. It is useful for binding, separating (puritying) and identifying immunoglobulin and for removing immunoglobulin molecules from serum. This is the coding sequence of one hybrid protein of the L protein. The hybrid proteins can bind all human immunoglobulin classes and many immunoglobulins from other species. They are highly soluble and retain their binding activity at high temperatures over a pH range of 3-10. They can be immobilised Gaps 9 1 AVENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDN 60 1 AVENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDN New protein L binding light chains of all immunoglobulin classes - for binding purifying and identifying immunoglobulin, also related DNA, vectors and host cells ; Length 434; Indels 100.0%; Score 1565; DB 14; 100.0%; Pred. No. 3.4e-110; ive 0; Mismatches 0;

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Gaps

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Indels

Length 467;

22;

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Expression vector; antibody binding protein; monoclonal antibody; Neo-R; B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Selecting monoclonal antibodies, by expressing them on the surface of hybridomas attached to antibody-binding protein, then reaction with antibody library -
                                                                                                                                                                                                                                                                                          100 GEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAE 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EFKGTFEEBATAEAYRYADLL-AKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIK 239
                                                                                                                                                                                              40 AVENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYEYADN
                                                                                                                                                                                                                                                                                                                                                                                          160 AYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AVENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDN
                                                                                                                                                                                                                                                                 61 GEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAE
                                                                                                                                                                                                                                                                                                                                                               121 AYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 ANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKV
                                                                          Score 1544.5; DB 2 Pred. No. 1.3e-108;
                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Moldenhauer G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Expression vector pSEX11L4 protein G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB10432 standard; Protein; 367 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 16; Fig 1; 22pp; German.
                                                                       98.78;
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                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-499832/45.
N-PSDB; AAA71428.
                                                                     Query Match
Best Local Similarity
                           467 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 DEKPE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11111
340 DEKPE 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-JUL-2000
                                                                                                                      Matches 303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB10432;
                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The specification describes a method for expressing and isolating a recombinant protein in a plant. The method comprising expressing a fusion protein including the recombinant protein and a callulose binding peptide fused to it, where the fusion protein is compartmentalised and sequestered within plant cells, plant derived tissue or cultured plant cells. The method is useful for obtaining large quantities of the recombinant proteins and protein products in a simple and cost-effective manner. Recombinant proteins may be used commercially, such as in the food processing industry, e.g. glucoamylases and glucose such as in the food processing industry, e.g. glucoamylases and glucose such as in the food processing industry, industry and for classes for isomercases for the hydrolysis of high molecular weight proteins and in manufacturing leather or alcoholic beverages, pectinesterases for pectin hydrolysis in food industry, lipases for cleaving expert linkage in triglycerides, and for effluent treatment. The recombinant proteins may further be used to produce protein antibiotics, which can be used in the alling processes, and to produce animal feed enzymes. The present sequence represents a fusion protein of the invention, and comprises a fusion of a cell signal peptide, protein L, CBD cex, and an endoplasmic reticulum retaining peptide.
240
                                                                                                241 NLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKVD 300
                                                                                                                                                                                            Protein production; food processing; protein antibiotic; feed enzyme; protein L: CBD cex protein; cell signal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of protein L/CBD cex/ER retaining peptide fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Expressing and isolating recombinant protein in a plant, useful for producing large quantities of recombinant proteins, by expressing a fusion protein including a cellulose binding peptide fused to a recombinant protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CBDT-) CBD TECHNOLOGIES LTD.
(YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB31372 standard; Protein; 467 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example; Fig 2a; 87pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shani Z, Shoseyov O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-112219/12.
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                                                                                                                                                                                                                                                                                            IIIII
EKPEE 305
                                                                                                                                                                                                                                                                 301 EKPEE 305
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Synthetic.

AAB31372;

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RESULT 3

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invention also describes antibody-binding proteins (I) that comprise a combination of the signal peptide of a murine immunoglobulin (Ig) kappa chain or a murine MHC (major histocompatibility complex) Class I k(k) molecule; an antibody-binding site of proteins A, G, L or LG, and the transmembrane domain of PDGFR (platelet-derived growth factor receptor) or CD52. The method is used to select MAD with specificity for particular antigens. MAD can be selected without separate culture of hybridomas, and selection can be made against many antigens in a library, optionally on the basis of strength of affinity for a particular antigen. Complex mixtures of hybridomas can be used for selection, reducing the time and cost involved in MAD selection. This sequence represents the protein G contained in the expression vector pSEXILL4 which contains the protein G, Neo-R and the bla protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                      200
                                                                                                                                                                                                                                                                                                                                           TFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIY 244
                                                                                                                                                                                                                                                                                                                                                      65 VDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAYRY 124
                                                                                                                                                                                                                                                                                                 125 ADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTOTAEFKG 184
                                                                                                                                                                                                                                   80
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                               64
                                                                                                                                                                                                                                                                                                                                                                                 5 KEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYT
                                                                                                                                                                                                                           Peptide; immunoglobulin; binding; analysis; purification; ELISA;
                                                                                                                                                                      Length 367;
                                                                                                                                                                      87.3%; Score 1366; DB 21;
88.6%; Pred. No. 2.8e-95;
                                                                                                                                                                                          15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60..968
/label- Mature protein L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PUBL-) PUBLIC HEALTH LAB SERVICE BOARD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36..59
/label= Signal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR42203 standard; Protein; 1027 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enzyme linked immunoabsorbant assay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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92GB-0026928
                                                                                                                                                                                         Matches 264; Conservative
                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptococcus magnus
                                                                                                                                                   367 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-MAY-1993;
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24-DEC-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein L.
                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR42203;
                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                         185
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180 AEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKE--KTPEEPKEEVT 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA 121
                                                                                                                                                                                                                                                  The synthetic immunoglobulin binding proteins derived from protein L correspond to the repeated sequences inprotein L which bind immunoglobulin kappa light chains. They can be used in protein analysis, purification procedures and other blochemical processes e.g. ELISA. The synthetic molecules are of particular advantage if they are free of regions in protein L which exhibit albumin and cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YRYADALKKDNGEYTVDVADKGYTLNIKFAGKE---KTPEEPKEEVTIKANLIYADGKTQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.4%; Score 1226.5; DB 14; Length 1027; 79.9%; Pred. No. 3.2e-84; ive 22; Mismatches 31; Indels 9; (
                                                                                                              immunoglobulin binding proteins derived from Protein {\tt L} - {\tt th} bind immunoglobulin kappa light chains but not albumin or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunoglobulin; binding; immobilisation; light chains;
Trowern AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibodies; diagnosis; pharmaceutical; ss.
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Alabel= Signal sequence. 60..968
/label= Mature protein L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein L.
Murphy JP,
                                                                                                                                                                                                          Disclosure; Figure 1; 28pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR43699 standard; Protein; 1027 AA
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Duggleby CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                        1993-368798/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                         1027 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298 KVDEKPEE 305
                                                              N-PSDB; AAQ50946
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                                                                                                                                                                                                                                                                                                                                                                      are free binding.
Atkinson A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Sim
Matches 246;
                                                                                                                                                            cell walls
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                      which
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70 KGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAYRYADALK 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKE--KTPEEPKEEVTIKANLIYA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EATAKAYAYANLLAKENGEYTADLEDGGNTINIKFAGKETPETPEEPKEEVTIKVNLIFA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KDNGEYTVDVADKGYTLNIKFAGKE--KTPEEPKEEVTIKANLIYADGKTQTAEFKGTFE 187
                                                                                                                                                                                                                                                                                                                                             L comprise repeated sequences from protein L which bind immunoglobulin kappa light chains. They can be used in protein analysis, purification procedures and other blochemical processes e. g. ELISA. The synthetic molecules are of particular advantage if they are free of regions in protein L which exhibit albumin and cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 ETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVAD 69
                                                                                                                                                                                                                                                                                                                             The synthetic immunoglobulin binding proteins derived from protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New immunoglobulin binding proteins derived from Protein L - which bind immunoglobulin kappa light chains but not albumin oʻr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Catalytic antibody; growth factor; B-cell mitogenesis; TLHL; L protein; hen egg lysozyme; kappa light chain; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Growth factor TLHL (catalytic antibody precursor).
                                                                                                                                       Murphy JP, Trowern AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77.7%; Score 1216; DB 1482.5%; Pred. No. 4.2e-84.ive 20; Mismatches 29
                                                                                                     (PUBL-) PUBLIC HEALTH LAB SERVICE BOARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric - Peptostreptococcus magnus.
Chimeric - Gallus sp.
Chimeric - Homo sapiens.
                                                                                                                                                                                                                                                                                             Claim 12; Figure 2; 28pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW32482 standard; Protein; 342
                 93WO-GB00950
                                                  92GB-0009804
92GB-0026928
                                                                                                                                       CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 241; Conservative
                                                                                                                                       Atkinson A, Duggleby
                                                                                                                                                                       WPI; 1993-368798/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                       N-PSDB; AAQ50947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09735887-A1
                 07-MAY-1993;
                                                  07-MAY-1992;
                                                                  24-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-MAR-1998
                                                                                                                                                                                                                                                           cell walls
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW32482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW32482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YRYADALKKDNGEYTVDVADKGYTLNIKFAGKE---KTPEEPKEEVTIKANLIYADGKTQT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKE--KTPEEPKEEVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide; immunoglobulin; binding; analysis; purification; ELISA; enzyme linked immunoabsorbant assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 14; Length 1027;
                                                                                                                                                                                                                                                                                                                        Protein L forms a complex with immunoglobulin Kappa light chain.
                                                                                                                                                                                                                         for prodn.
                                                                                                                                                                                                                                                                                                                                          Purified protein can be used as a reagent for immobilising antibodies e.g. on columns, in diagnostic tests and in assays. may also be used in the production of pharmaceuticals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
                                                                                                                                                                                                                      Immunoglobulin binding polypeptide, protein L - used for pi
of pharmaceuticals and for immobilising antibodies e.g. on
columns, in diagnostic tests and in assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunoglobulin binding protein derived from protein L.
                                                                                                                                     Duggleby CJ, Murphy JP, Trowern AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.4%; Score 1226.5; DB ... 79.9%; Pred. No. 3.2e-84; iive 22; Mismatches 31.
                                                                                                    (PUBL-) PUBLIC HEALTH LAB SERVICE BOARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR42204 standard; Protein; 291 AA
                                                                                                                                                                                                                                                                                           Claim 4; Figure 1; 29pp; English
                                 93WO-GB00949.
                                                                  92GB-0009804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 79.9
Matches 246; Conservative
                                                                                                                                                                      WPI; 1993-368797/46.
                                                                                                                                                                                                                                                                                                                                                                                                                1027 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298 KVDEKPEE 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---EQPGE 578
                                                                                                                                                                                      P-PSDB; AAR43699
                                                                                                                                     Atkinson A,
                                 07-MAY-1993;
                                                                  07-MAY-1992:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-MAY-1994
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11-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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Gallus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1,
                                                                                                                                                                                                                                                                                                                     This protein comprises growth factor TLHL, where L is the immunoglobulin binding entity from Peptostreptococcus magnus, H is residues 42-62 of hen eagy lysozyme, and T represents the variable kappa light chain (see AAM32483) from human myeloma protein LEN.

Was expressed in E. coli DH10B cells utilising a DNA construct (see AAT91598) produced from LHL (see AAT91986), kappa (see AAT91590) and synthetic linker oligonucleotides, and was purified from total bacterial lysate via a strep-tag. The linker contains a cleavage is the for tobacco etch virus (TPV) protease. TLHL was designed so that the kappa portion of the protein is cleaved by TEV protease into 'T' and 'LHL' moieties. Production of catalytic antibodies to a specific antigen comprises administering to an animal a growth factor comprising an antigen capable of interacting with a B cell bound catalytic antibody. The antigen is fused to a B cell surface molecule binding protein for the antigen to be cleaved and for the remainder of the molecule to induce B cell mitogenesis (claimed). LHL crosslinks with surface immunoglobulin on B cells. This induces be cell activation and blast formation. Internalisation and processing of LHL leads to the presentation of the H peptide signals the child contains and contains and undergo antibody class switching activated B cell intogralication of the H peptide signals the activated B cell intogralication and undergo antibody class switching and contains the activated B cell intogralication and undergo antibody class switching and contains the activated B cell intogralication and undergo antibody class switching and contains the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Growth factor precursor; B-cell surface; T cell surface; CAb; hepatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----PKEEVTIKANLIYADGKTQTAEFKGTFE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |||||||| |
IKFAGKEATNRNTDGSTDYGILQINSRWGGLTSAEEVTIKANLIFANGSTQTAEFKGTFE 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLN 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and secretion. The catalytic antibodies generated by the process can have diagnostic and therapeutic applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
                                                                                                                                                                                                                                          New catalytic antibody precursors - comprising a B-cell surface molecule binding portion which can induce B-cell mitogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 18; Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EATAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPK 161
                                                                                                                                                        Tarlinton DM, Treutlein HR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 618; DB 1
Pred. No. 6e-39;
5; Mismatches
                                                                                                                                                                                                                                                                                          66-68; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY06909 standard; Protein; 342 AA.
                                                                                                                      (AMRA-) AMRAD OPERATIONS PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.5%;
75.9%;
                                                                                    96AU-0008951.
                                 97WO-AU00194
                                                                   97AU-0005375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLHL amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IKFAGKEKTPEE-----
                                                                                                                                                      Suess GM,
                                                                                                                                                                                        WPI; 1997-489572/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity
Matches 126; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             342 AA;
                                                                                                                                                                                                                                                                                          Example 11; Page
                                                                                                                                                                                                        N-PSDB; AAT91589
                                                                   27-FEB-1997;
                                                                                     26-MAR-1996;
                                                                                                                                                        Koentgen F,
02-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY06909;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234
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The invention relates to a growth factor precursor that comprises B-cell surface binding part, antibody (CAb); and a peptide comprising heavy and light challed antibody (CAb); and a peptide comprising heavy and light chalms of immunoglobulin. When the antigen is cleaved the B cell surface part can interact with its target. The growth factor precursors are used to select B cells that produce Ag-specific CAb, and to generate CAb from such cells (by inducing mitogenesis, caused by the growth factor released by specific cleavage). The Ag-specific CAb can be directed against, e.g. tumour necrosis factor (treatment of rheumatoid arthritis or toxic shock syndrome); viral docking receptors (treatment of human immune virus, hepatitis and influenza infections); tumour-specific antigens; amyloid plaque (treatment of Alzheimer's disease or myeloman) or IGE (treatment of allergies such as asthma). CAD may also be used for drug detoxification, contraction as asthma). CAD may also be used for drug detoxification, contraction in a viral or other gene therapy vector. The particularly the growth factor precursors are produced by delivering the prowth factor or ordersponding nucleic acid in a viral or other gene therapy vector. The present sequence represents the amino acid sequence of TLHL. The LHL is a growth factor comprising H flanked by two L molecules where L is a B cell surface molecule binding portion from hore general cell, virus) sensitive competitive comprises the sequence region.
rheumatoid arthritis; toxic shock syndrome; viral docking receptor; human immune virus; tumour-specific antigen; amyloid biaque; myeloma; Alzheimer's disease; IGE; allergy; asthma; drug detoxification; autoimmune; inflammatory disease; gene therapy; protein L; P. magnus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --PKEEVTIKANLIYADGKTQTAEFKGTFE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 SEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLN 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Growth factor precursor cleaved by antigen-specific catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39.5%; Score 618; DB 20; Length 342; 75.9%; Pred. No. 6e-39; 1.ve 5; Mismatches 15; Indels 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EATAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treutlein HR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 11; Page 67-69; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tarlinton DM,
                                                                                                                                                                    hen egg lysosyme; HEL; LHL; TLHL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMRA-) AMRAD OPERATIONS PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-AU00783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97AU-0009306
                                                                                                                                                                                                                                                    Peptostreptococcus magnus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 126; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Koentgen F, Suess GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-244394/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAX34592
                                                                                                                                                                                                                                                                                                                                                                  WO9915563-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .8-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-SEP-1997;
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This polypeptide comprises growth factor LHL-omp, where L is the immunoglobulin binding entity from Peptostreptococcus magnus and H is residues 42-62 of hen egg lysozyme. It was generated from is residues 42-62 of hen egg lysozyme. It was generated from LHL.seq (see AAW32481) such that the E. coli ompA signal sequence (generated by purifying LHL.seq from whole bacterial host cells) was eliminated. The N-terminal omp peptide found in LHL (see AAW32482), LHL.seq (see AAW32481) and TLHL (see AAW32482) induces multimerisation as demonstrated by a potentiation of biological activity as compared to recombinant LHL-omp. Production of catalytic antibodies to a specific antigen comprises administering to an animal a growth factor comprising an antigen capable of interacting with a B cell bound catalytic antibody. The antigen is fused to a B cell surface molecule binding protein for the antigen to be cleaved and for the remainder of the molecule to induce B cell mitogenesis (claimed). The observation that omp induces multimerisation allows the design of simpler molecules with the same desired biological function as the contraction by the process can have diagnostic and therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New catalytic antibody precursors · comprising a B-cell surface molecule binding portion which can induce B-cell mitogenesis
                                                                                                                                                                    Catalytic antibody; growth factor; B-cell mitogenesis; LHL-omp; L protein; hen egg lysozyme; HEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 615; DB 18; Length 178;
Pred. No. 4.5e-39;
5; Mismatches 14; Indels 20
                                                                                                                                  Growth factor LHL-omp (catalytic antibody precursor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treutlein HR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tarlinton DM,
                                                                                                                                                                                                                                                                                                             /note= "FLAG epitope"
170..178
                                                                                                                                                                                                                      Chimeric - Peptostreptococcus magnus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 27; Page 76; 109pp; English.
                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                            /note= "strept-tag"
                                AAW32486 standard; Protein; 178 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMRA-) AMRAD OPERATIONS PTY LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97AU-0005375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96AU-0008951
                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suess GM,
                                                                                                                                                                                                                                      Chimeric - Gallus sp.
Chimeric - Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-489572/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAT91591
                                                                                                                                                                                                                                                                                                                                                                                            W09735887-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             applications
                                                                                                  27 - MAR - 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Koentgen F,
                                                                                                                                                                                                                                                                                                                                                                                                                              02-OCT-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence
                                                                AAW32486;
                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                          Peptide
RESULT 10
                AAW32486
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The invention relates to a growth factor precursor that comprises B-cell surface binding part, antigen cleavable by a catalytic antibody (CAB); and a peptide comprising heavy and light chains of immunoglobulin. When the antigen is cleaved the B cell surface part can interact with its target. The growth factor precursors are used to select B cells that produce Ag-specific CAB, and to generate CAB from such cells (by inducing mitogenesis, caused by the growth factor released by specific cleavage). The Ag-specific CAB can be directed against, e.g. tumour necrosis factor (treatment of rheumatoid arthritis or toxic shock syndrome); viral docking receptors (treatment of human immune virus, hepatitis and influenza infections); tumour-specific antigens; amyloid plaque (treatment of Alzheimer's disease or myeloma) or IGE (treatment of alleques such as astima). CAB may also be used for drug detoxification, to treat autoinmune or inflammatory diseases and to eliminate environmental or industrial pollutants, such as plastics and petroleum. Particularly the growth factor precursors are produced by delivering the corresponding nucleic actid in a viral or other gene therapy vector. The present sequence represents the amino acid sequence of the LHL growth factor carrying an omph signal peptide (LHL.omp). L is a B cell surface molecule binding portion from hen egg lysosyme (HEL). LHL is a growth factor comprising H flanked by two L molecules.
                                                                                                                                                                                                                                                                                                                                                                                                      Growth factor precursor; B-cell surface; T cell surface; CAb; hepatitic catalytic antibody; immunoglobulin; tumour necrosis factor; influenza; rheumatoid arthritis; toxic shock syndrome; viral docking receptor; human immune virus; tumour-specific antiqen; amyloid plaque; myeloma; Alzheimer's disease; IGE; allergy; asthma; drug detoxification; autoimmune; inflammatory disease; gene therapy; protein L; P. magnus;
-PKEEVTIKANLIYADGKTQTAEFKGTFEEA 117
                                          72 FAGKEATNRNTDGSTDYGILQINSRWGGLTSAEEVTIKANLIFANGSTQTAEFKGTFEKA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Growth factor precursor cleaved by antigen-specific catalytic
                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of a form of LHL growth factor (LHL.omp).
                                                                                                           118 TAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Koentgen F, Suess GM, Tarlinton DM, Treutlein HR;
                                                                                                                                                                                                                                      AAY06913 standard; Protein; 178 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Examples; Page 74; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AMRA-) AMRAD OPERATIONS PTY LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-AU00783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hen egg lysosyme; HEL; LHL.
                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptostreptococcus magnus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-244394/20.
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78 FAGKEKTPEE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus sp.
                                                                                                                                                                                                                                                                              AAY06913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibody
                                                                                                                                                                                             RESULT 11
                                                                                                                                                                                                               AAY06913
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EEVIIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLNIK 77

39.3%; 76.2%;

Conservative

Matches 125;

12

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Query Match

Similarity

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WPI; 1999-244394/20
                                                                                                    198 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Koentgen F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus sp.
                                                                                                      Sednence
                                                                                                                                                                                                                                                                                                                       AAY06910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibody
                                                                                                                                                                                                                                                                                RESULT 13
AAY06910
ID AAY069
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                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunoglobulin binding entity from Peptostreptococcus magnus and H is residues 42-62 of hen egg lysozyme. It is a modified form of LHL (see AAW32479) having an N-terminal FLAG epitope (see AAW32484) and a C-terminal strep-teg (see AAW32485) that facilitates purification. Production of catalytic antibodies to a specific antigen comprises administering to an animal a growth factor comprising an antigen capable of interacting with a B cell bound catalytic antibody. The antigen is fused to a B cell surface molecule binding protein for
                                                                                                    78 FAGKEKTPEE--------PKEEVTIKANLIYADGKTQTAEFKGTFEEA 117
                                                                                                              Gaps
                                                             EEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLNIK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This polypeptide comprises growth factor LHL.seg, where L is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New catalytic antibody precursors - comprising a B-cell surface molecule binding portion which can induce B-cell mitogenesis
                                             20;
                                                                                                                                                                                                                                                                                 Catalytic antibody; growth factor; B-cell mitogenesis; LHL.seq; L protein; hen egg lysozyme; HEL.
                        Length 178;
                                             Indels
                                                                                                                                                   118 TAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPK 161
                                                                                                                                                                                                                                                                Growth factor LHL.seq (catalytic antibody precursor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tarlinton DM, Treutlein HR;
                         Score 615; DB 20;
Pred. No. 4.5e-39;
                                            5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Page 70-71; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                          /note= "FLAG epitope"
190..198
                                                                                                                                                                                                                                                                                                             Chimeric - Peptostreptococcus magnus
                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
22..29
                                                                                                                                                                                                                                                                                                                                                                                       /note= "strept-tag"
                                                                                                                                                                                                          ₽.
                                                                                                                                                                                                         AAW32481 standard; Protein; 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATIONS PTY
                         39.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96AU-0008951.
                                                                                                                                                                                                                                                                                                                                                                                                                                             97WO-AU00194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                97AU-0005375
                                                                                                                                                                                                                                            27-MAR-1998 (first entry)
                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suess GM,
                                                                                                                                                                                                                                                                                                                      - Gallus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-489572/45.
                                   Best Local Similarity
       178 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAT91588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMRA-) AMRAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Koentgen F,
                                                                                                                                                                                                                                                                                                                                                                                                                          02-OCT-1997
                                            Matches 125;
                                                                                                                                                                                                                                                                                                                      Chimeric
Chimeric
        Sequence
                         Query Match
                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                            Peptide
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Growth factor precursor; B-cell surface; T cell surface; CAb; hepatitis; catalytic antibody; immunoglobulin; tumour necrosis factor; influenza; rheumatoid arthritis; toxic shock syndrome; viral docking receptor; human immune virus; tumour-specific antigen; amyloid plaque; myeloma; Alzheimer's disease; IGB; allergy; asthma; drug detoxification; autoimmune; inflammatory disease; gene therapy; protein L; P. magnus; hen egg lysosyme; HEL; LHL; LHL.seq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a growth factor precursor that comprises B-cell surface binding part, T cell surface binding part, antigen cleavable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the antigen to be cleaved and for the remainder of the molecule to induce B cell mitogenesis (claimed). LHL.seq has the same biological activity as LHL, which crosslinks with surface immunoglobulin on B cells. This induces B cell activation and blast formation. Internalisation and processing of LHL leads to the presentation of the H peptide on MHC II. T cell recognition of MHC II with the H peptide signals the activated B cell to proliferate and undergo antibody class switching and secretion. The catalytic therapeutic applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----PKEEVTIKANLIYADGKTQTAEFKGTFEEA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 EEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLNIK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 EEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLNIK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Growth factor precursor cleaved by antigen-specific catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of a form of LHL growth factor (LHL.seq).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 TAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treutlein HR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 615; DB 18;
Pred. No. 5.1e-39;
5; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tarlinton DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Page 70-71; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY06910 standard; Protein; 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.3%;
76.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AMRA-) AMRAD OPERATIONS PTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 39.3
Best Local Similarity 76.2
Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FAGKEKTPEE------
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by a catalytic antibody (CAb); and a peptide comprising heavy and light chains of immunoglobulin. When the antigen is cleaved the B cell surface part can interact with its target. The growth factor precursors are used to select B cells that produce Ag-specific Cab, and to generate CAb from such cells (by inducing mitogenesis, caused by the growth factor released by specific cleavage). The Ag-specific Cab can be directed against, e.g. tumour necrosis factor (treatment of rhemmatoid arthritis or toxic shock syndrome); viral docking receptors (treatment of human immune virus, hepatitis and influenza infections); tumour-specific antigens; amyloid plaque (treatment of Alzheimer's disease or myeloma) or IGE (treatment of plaque (treatment of Influenza infections); tumour-specific antigens; amyloid place (treatment of Influenza infections); tumour-specific antigens; amyloid place (treatment of Influenza infections); tumour-specific antigens; amyloid place (treatment of Influenza infections); tumour-specific antigens, amyloid perticularly the growth factor precursors are produced by delivering the corresponding nucleic acid in a viral or other gene therapy vector. The present sequence represents the amino acid sequence of the LHL growth factor arrying a N-terminal FLAG epitope and a C-terminal strep tag. I is a B cell surface molecule binding portion from protein Loft of Pysosyme (HEL). LHL is a growth factor comprising H flanked by two L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 FAGKEKTPEE--------PKEEVTIKANLIYADGKTQTAEFKGTFEEA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 EEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLNIK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 EEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLNIK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Catalytic antibody; growth factor; B-cell mitogenesis; LHL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Growth factor CATAB-TEV (catalytc antibody precursor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 TAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treutlein HR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 615; DB 20;
Pred. No. 5.1e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L protein; hen egg lysozyme; kappa light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tarlinton DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric - Peptostreptococcus magnus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW32480 standard; Protein; 495 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMRA-) AMRAD OPERATIONS PTY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97WO-AU00194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric - Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Suess GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-489572/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                        198 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAT91587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Koentgen F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                       molecules
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binding entity of Peptostreptococcus magnus, H is residues 42-62 of then egg lysozyme, and T represents the variable kappa light chain (see AAW32483) from human myeloma protein LEN; and (b) an additional, C-terminal kappa protein, the elements of CATAB-TEV being joined by protease. CATAB-TEV was designed so that the kappa portions of the proteins. CataB-TEV was designed so that the kappa portions of the proteins. Production of catalytic antibodies to a specific antigen comprises administering to an animal a growth factor comprising an entibody. The antigen to be cleased to a secific antigen antipody. The antigen is fused to a B cell surface molecule binding protein for the antigen to be cleaved and for the remainder of the molecule to induce B cell mitogenesis (claimed). LHL (see CaPAB-TEV) crosslinks with surface immunoglobulin on B cells. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Growth factor precursor; B-cell surface; T cell surface; CAb; hepatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     catalytic antibody; immunoglobulin; tumour necrosis factor; influenza; rheumatoid arthritis; toxic shock syndrome; viral docking receptor; human immune virus; tumour-specific antigen; amyloid plaque; myeloma; Alzheimer's disease; IGE; allerapy; asthma; drug detoxification; autoimmune; inflammatory disease; gene therapy; protein L; P. magnus; hen egg lysosyme; HEL; LHL; CATAB-TEV; tobacco etch virus; TLHL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 IKFAGKEKTPEE--------PKEEVTIKANLIYADGKTQTAEFKGTFE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              induces B cell activation and blast formation. Internalisation and processing of LHL leads to the presentation of the H peptide on MHC II. T cell recognition of MHC II with the H peptide signals the activated B cell to proliferate and undergo antibody class switching and secretion. The catalytic antibodies generated by the process can have diagnostic and therapeutic applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 SEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLN 75
                                                                                                                        This polypeptide comprises CATAB-TEV, a synthetic growth factor composed of: (a) TLHL (see AAW91589), where L is the immunoglobulin
               New catalytic antibody precursors - comprising a B-cell surface molecule binding portion which can induce B-cell mitogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   294 KATSEAYAYADTLKKDNGEYTVDVADKGYTLNIKFAGKE 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 614; DB 18;
Pred. No. 1.9e-38;
4; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 EATAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKE 154
                                                                              Claim 12; Page 61-63; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY06908 standard; Protein; 495 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATAB-TEV aminoacid sequence.
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78.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptostreptococcus magnus
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Matches 125; Conserv
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The invention relates to a growth factor precursor that comprises B-cell surface binding part, antigen cleavable by a catalytic antibody (CAb); and a peptide comprising heavy and light chains of immunoglobulin. When the antigen is cleaved the B cell surface part can interact with its target. The growth factor precursors are used to select B cells that produce Ag-specific CAb, and to generate CAb from such cells (by inducing mitogenesis, caused by the growth factor released by specific cleavage). The Ag-specific CAb can be directed against, e.g. thmour necrosis factor (treatment of Appending arthritis or toxic shock syndrome); viral docking receptors (treatment of human immune virus, hepatitis and influenza infections); tumour-specific antigens; amyloid allergies such as asthma). CAb may also be used for drug detoxification, to treat autoimmune or inflammatory diseases and to eliminate allergies such as asthma). CAb may also be used for drug detoxification, to treat autoimmune or inflammatory diseases and to eliminate corresponding nucleic acid in a viral or other gene therapy vector. The particularly the growth factor precursors are produced by delivering the corresponding nucleic acid in a viral or other gene therapy vector. The present sequence represents the amino acid sequence of CAPTAB-TEV which is assembled from TLHI and kappa by PCR. The LLL is a growth factor comprising H flanked by two molecules where L is a B cell surface molecule binding portion from protein L of P. magnus; H is a T cell surface molecule binding portion from hen egg lysosyme (HEL). THH is cut in the Linked to kappa chain via TEV (tobacco etch virus) sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ij
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                                                                                                                                              Koentgen F, Suess GM, Tarlinton DM, Treutlein HR;
                                                                                                                                                                                                                                                                                                                                       Example 15; Page 64-66; 101pp; English.
                                                                                               (AMRA-) AMRAD OPERATIONS PTY LTD.
                                                  97AU-0009306
  98WO-AU00783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 78.69
Matches 125; Conservative
                                                                                                                                                                                              WPI; 1999-244394/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                495 AA;
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18-SEP-1998;
                                                  19-SEP-1997;
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                                                                                                                                                                                                                                                                                             antibody
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16 SEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLN 75

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...-----PKEEVTIKANLIYADGKTQTAEFKGTFE 115

76 IKFAGKEKTPEE-----

EATAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKE 154

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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 protein search, using sw model OM protein October 29, 2002, 09:25:26; search time 10.571 Seconds (without alignments) 1589.653 Million cell updates/sec Run on:

US-08-325-278B-3 2235 Title: Perfect score:

1 AVENKEETPETPETDSEEEV.......GVDGVWTYDDATKTFTVTEM 434 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

staphylococ bacillus su homo sapien saccharomyc streptococc oryctolagus bacillus sp notophthalm caro neisseria m saccharomyc P19909 streptococc streptococc staphylococ homo sapien bacillus an rattus norv rattus norv mus musculu homo sapien streptococc gallus gall cyprinus ca gallus gall staphylococ sapien bacillus su mus musculu dictyosteli bos taurus salmonella daucus homo Description P21333 P21333 P43597 P435597 P48553 P490553 P15839 P15839 P15839 P15839 P165952 P056968 P056968 P056968 P16933 P16 P06654 Q53654 P07197 P20075 P80544 P16397 Q28641 P38537 Q91145 P25062 SUMMARIES NFM_HUMAN BRSP_SAUCA BRSP_STADU SUBE_BACSU ABP2_HUMAN YF16_YEMST DEXT_STROO WAPA_BACSU WAPA_BACSU NFM_MOUSE SLA1_BACAN NFM_RAT SPG2_STRSP SPG1_STRSP CNA_STAAU MAPB_RAT MAPB_MOUSE MAPB_HUMAN SSP5_STRGN MYH3_CHICK MYSS_CYPCA NFM_BOVIN FLJB_SALTY TBB2_NEIMB NFM_CHICK FNBA_STAAU MYS2_DICDI NEBU_HUMAN IF3X_YEAST MYH4_RABIT SLAP_BACSH COLA_CLOPE DB Query March Length 814 845 2464 2466 1266 1150 11935 11935 11018 11104 11104 11104 11104 11104 555 1637 1433 2647 1233 1337 2334 848 Score Result Š

halobacteri

CA1C_NOTVI CSG_HALVO

P06546 bacillus br P54938 oryctolagus Q08372 plasmodium Q02113 bacillus su P09405 mus musculu P08198 halobacteri P38538 bacillus br P16271 lactococcus R15292 lactococcus Q99715 homo sapien P06180 xenopus lae P43261 escherichia	
SLPM BACBR NFM_RABIT S230_PLAFO CWBA_BACSU NUCL_MOUSE CSG_HALHA S1PH_LACLC P3PL_LACLC P3P_LACLC CACL_HUMAN HIBN XENLA EAE_ECO57	
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ALIGNMENTS

RESULT	RESULT 1
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2 E	(Rel
DI	(Rel.
T E	ition update)
S C	immunogrobutin e binaing procein e precursor (ise binaing procein e). SPG.
os	Streptococcus sp. (strain G148).
88	Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
ပ	
X O	NCBL_TaxID=1306;
Y C	
д Т Г	SEQUENCE FROM N.A.
2 X	SIRAIN-G140; MEDLINE-88029445: PubMed=3665928:
RA	Olsson A., Eliasson M., Guss B., Nilsson B., Hellman U.,
RA	Lindberg M., Uhlen M.;
\mathbf{RT}	"Structure and evolution of the repetitive gene encoding
RT	streptococcal protein G.";
X G	Eur. J. Blocnem. 108:319-324(198/).
N C	[4] CPJIENCE DEOM N N
ת ה	SENDATURE FOR N.A.
X X	JINGHITH GA. 000; MEDITUNE RROLLER DIDMAGA 3458689.
RA.	Filpula D., Alexander P., Fahnestock S.R.;
RT	"Nucleotide sequence of the protein G gene from Streptococcus GX7805,
RŢ	and comparison to previously reported sequences.";
R.	Nucleic Acids Res. 15:7210-7210(1987).
N I	[3]
R.P	SEQUENCE OF 114-593 FROM N.A.
א נ	3.TKG118 = G.48 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5
4 4	H [emargo], N- A form M acidin
RA	
RT	"Structure of the IgG-binding regions of streptococcal protein G.";
RL	•
RN	[4]
RP	STRUCTURE BY NMR OF 371-427.
RC	STRAIN=G148;
ZX.	MEDLINE=98290449; PubMed=9628485;
RA	
RT	"Design, structure and stability of a hyperthermophilic protein
H I	Variant; Variant;
3 5	Nat. Stiller bill 1944/0-4/3/19940)
ט ני	: SOBCEDIOLEN DOCATION: 17PE 1 MEMORINE PIOCETH. CELL WALL.
8 8	IN THE RECTION OF THE MEMBRANE ANCHOR.
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ပ္ပ	This SWISS-PROT entry is copyright. It is produced through a collaboration
ပ္ပ	between the Swiss Institute of Bioinformatics and the EMBL outstation
ပ္ပ	the European Bioinformatics Institute. There are no restrictions on its
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ပ္ပ	modified and this statement is not removed. Usage by and for commercial
၁	entities requires a license agreement (See http://www.isb-sib.ch/announce

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PIR; A24496; A24496.
PDB; 1PGA; 30-APR-94.
PDB; 1PGB; 30-APR-94.
PDB; 1PGX; 15-JUL-92.
       SPG1_STRSP
               17;
                                                                                                                                                                                                                                             SURFACE
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                                  R PIR; A26314; A26314.

R PIR; A26314; A26314.

R PIR; A26314; A26314.

R InterPro; IPR001899; Gram_pos_anchor.

R InterPro; IPR001899; Gram_pos_anchor.

R Pfam; PF0176; Gram_pos_anchor; 1.

R Pfam; PF0178; IgG_binding_B; 3.

R Pfam; PF0378; IgG_binding_B; 3.

R PROSITE; PS00313; GROSANCHOR.

M IgG-binding protein; Repeat; Transmembrane; Cell wall; Signal;
                                                                                                                                                                                                                                                                                                               ----KTQTAEFKGTFEEATAEAYRYADALKKDNGE---YTVDVADKGYTLNIKFAGKEK
                                                                                                                                                                                                                                                                                                                                                   160 LSDFLKSQTP-----AEDTVKSIELAEAKVLANRELDKYGVSDYHKNLINNAKTVEGVK
                                                                                                                                                                                                                                                                                                                                                                           YTVDVADKGYTLNIK-FAGKEKTPEE----PKEEVTIKANLIYADGKTQTAEFKGTFAE
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5 X 5 AA REPEATS OF [DE]-D-A-K-K.
CONSERVED IN GRAM-POSITIVE COCCI
                                                                                                                                         IMMUNOGLOBULIN G BINDING PROTEIN :
EXTRACELLULAR (POTENTIAL).
MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                        31.7%; Score 708; DB 1; Length 593; 48.3%; Pred. No. 1.2e-31; Indels 131; Indels
                                                                                                                                                                                                                                                           048BAA760D5B2920 CRC64;
                                                                                                                                                                   CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                37 AA REPEATS.
                                                                                                                                                                                                              55 AA REPEATS
or send an email to license@isb-sib.ch)
                                                                                                                                                                        ALA-RICH.
                                                                                                                                                                                                                                                           63291 MW;
            EMBL; X06173; CAA29540.1; -. EMBL; Y00428; CAA68489.1; -. EMBL; X04015; CAA27638.1; -.
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Matches 205; Conserv
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                        01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Immunoglobulin G binding protein G precursor (IGG binding protein G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRUCTURE BY NMR OF 298-351.
MEDLINE=91335209; PubMed=1871600;
Gronenborn A.M., Filpula D.R., Essig N.Z., Achari A., Whitlow M., Wingfield P.T., Clore G.M.;
Mingfield P.T., Clore G.M.;
A novel, highly stable fold of the immunoglobulin binding domain of streptococcal protein G.";
Science 253:657-661(1991).
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Butterworth S., Lamzin V.S., Wigley D.B., Derrick J.P., Wilson K.S.; Submitted (APR-1997) to the PDB data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ***AXY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF 297-352.
MEDLINE=95308043; PubMed=7788293;
Sauer-Eriksson A.E., Kleywedt G.J., Uhlen M., Jones T.A.;
Crystal structure of the C2 fragment of streptococcal protein G in complex with the Fc domain of human 196.";
                                                                                                                                                                                                                                                                    Streptococcus sp. (Lancefield group G).
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Type I membrane protein, Cell wall. SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS IN THE REGION OF THE MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallagher T., Alexander P., Bryan P., Gilliland G.L.; "Two crystal structures of the B1 Immunoglobulin-binding domain streptococcal protein G and comparison with NMR."; Biochemistry 33:4721-4729(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           m streptococcal protein G. An of the structure alone and in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fahnestock S.R., Alexander P., Nagle J., Filpula D.; "Gene for an immunoglobulin-binding protein from a group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.07 ANGSTROMS) OF 228-282
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           448 AA
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Derrick J.P., Widley D.B.;
The third Igg-binding domain from analysis by X-ray crystallography ocomplex with Fab.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-86304178; PubMed=3745123; Fahnestock S.R., Alexander P., Na
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteriol. 167:870-880(1986).
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               STANDARD;
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SPG1_STRSP
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NCBI_TaxID=1280;
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Best Local Simi
Matches 136;
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CONSERVED IN GRAM-POSITIVE COCCI SURFACE
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                                                                                                                                                                                                                                                                                                                                                                                   LIYA-DG-----KTQTAEFKGTFAEATAEAYRYAD---LLAKENGKYTADLEDGGYTINI 292
                                                                                                                                                                                                                                                                                                                                                                                                 153 ISEATDGLSDFLKSQTP----AEDTVKSIELAEAKVLANRELDKYGV----SDYHKNL 202
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                                                                                                                                       IMMUNOGLOBULIN G BINDING PROTEIN G.
                                                                                                                                                                                                                                                                                               48;
                                                                                          PRINTS; PR00015; GPOSANCHOR.
PROSITE; PS00343; GRAM_POS_ANCHORING; 1.
IgG-binding protein; Repeat; Transmembrane; Cell wall; Signal;
                                                                                                                                                                                                                                                                             30.6%; Score 683; DB 1; Length 448; 53.2%; Pred. No. 1.9e-30; Live 15; Mismatches 92; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
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(Rel. 37, Last sequence update)
(Rel. 40, Last annotation update)
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                                                                                                                                                 EXTRACELLULAR
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                                         InterPro; IPR002988; GA.
InterPro; IRR01899; Gram_pos_anchor.
InterPro; IPR000724; IgG_bind_B.
Pfam; PF01468; GA; 2.
                                                                            Pfam; PF00746; Gram_pos_anchor; 1. Pfam; PF01378; IgG_binding_B; 2.
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29-JUL-98.
20-JUL-95.
15-APR-93.
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15-DEC-1998
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MEMBRANE ARCHOR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
COLLAGEN-BINDING. Indels B6A1CC072E575D76 CRC64; Interpro: IPR001899; Gram_pos_anchor. PROSITE; PS00343; GRAM_POS_ANCHORING; FALSE_NEG. Signal; Repeat; Transmembrane; Cell wall; 3D-structure. Symersky J., Patti J.M., Carson M., House-Pompeo K., Moore D., Jin L., Schneider A., DeLucas L.J., Hoeoek Narayana S.V.L.; DB 1; Mismatches 166; X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 169-318 MEDLINE=97475225; PubMed=9334749; COLLAGEN ADHESIN. 8.4%; Score 188.5; DB 3.8%; Pred. No. 0.0032 or send an email to license@isb-sib.ch). POTENTIAL. Lindberg M., Hoeoek M.; J. Biol. Chem. 269:11672-11672(1994) Biol. Chem. 267:4766-4772(1992). COLLAGEN-CONTAINING SUBSTRATA. STRAIN=FDA 574; MEDLINE=92165839; PubMed=1311320; MEDLINE-94032261; PubMed-8218209; 133066 MW; 61; EMBL; M81736; AAA20874.1; -. 23.8%; Conservative COLLAGEN-BINDING DOMAIN Lindberg M., Hoeoek M.; 1093 1157 1156 1183 1157 1177 1093 1183 1AMX; 24-JUN-98. ¥¥; Similarity SEQUENCE FROM N.A. aureus adhesin."; 1183 533 1093 1151 STRAIN-FDA 574;

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          OF AXONAL CALIBER.

PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.
SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             541 GAKS-DQAEEG-----GSEKEGSSEKEEGE-----QEEGETE-AEAEG--EEAEAK 582
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Pred. No. 0.13;
56; Mismatches 153; Indels 172;
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COIL 2B.
6 x 13 AR TANDEM REPEATS.
0-LINKED (GLCNAC) (BY SIMILARITY).
0-LINKED (GLCNAC) (BY SIMILARITY).
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LINKER 1.
COIL 1B.
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Matches 117; Conservative
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A30157; A30157
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                                                                                                                                                                                                                                                                                                                                               MADI. Gen. Genet. 218:143-151(1989).
-!- FUNCTION: MAY PLAY A ROLE IN LATE EMBRYOGENY.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC, PROTEIN BODIES, AND CELL WALLS
OF ZYGOTIC EMBRYO AND ENDOSPERM TISSUE.
                       864
                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids II; Apiales, Apiaceae, Daucus.
NCBI_TaxID=4039;
                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: SOME, TO COTTON LEA D7, TO RAPE LEA 76, AND CARROT DC-3.
--TFTVTEKPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNG
             Z.R.;
DC 8, from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 155; DB 1; Length 555;
Pred. No. 0.083;
                                                                                                                                                                                                                                                                                                               Franz G., Hatzopoulos P., Jones T.J., Krauss M., Sung
"Molecular and genetic analysis of an embryonic gene,
Daucus carota L.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D15E8A30E51BD1AB CRC64;
                                                                                                                                                01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-MAY-2000 (Rel. 39, Last annotation update)
Embryonic protein DC-8 (Clone 8/10).
                                                                                                                           555 AA.
                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                        STRAIN-CV. QUEEN ANNE'S LACE;
MEDLINE-89384429; PubMed-2571069;
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11.
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16.
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                    818 KGSGREEEKGVVTNGLDLSPA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X16131; CAA34258.2; -.
                                            416 VDGVWTYDDATKTFTVTE 433
                                                                  GDGATKY -- ITKSVTVTQ 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEA.
                                                                                                                           STANDARD;
                                                                                                                                                                                                          Daucus carota (Carrot).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              303
325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S04909; S04909.
InterPro; IPR004238;
Pfam; PF02987; LEA; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              555 AA;
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDC8_DAUCA P20075;
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                                                                                                    RESULT 5
EDC8_DAUCA
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18;

Gaps

96;

57; Mismatches 187; Indels

6.98;

23.9%;

Best_Local Similarity 23.9 Matches 107; Conservative

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                             297
                                                                                                                                              87 DYAYDKGREGGDVAAQKAEEAKEKAKMAKDTIMGKAGEYKDYTAQKA-----EEAKEKA 140
                                                                                                                                                                                               122 YRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKT---PEEPKEEVTIKANLIYADGKTQ 178
                                                                                                                                                                                                                                                                                                                                              191 TAQKAAEAKEKTGE---YKDYAAQKAAEAKVLAAQKA-----AEAKDTTGKDGEYKDYA 241
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                                                                                             EYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA 121
61
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STRAIN-ISOLATE 1061;
Savolainen K., Kuusela P., Paulin L., Korhonen T.K.;
"Pls, a large repeat-rich surface protein of methicillin resistant
                                                                                                                                                                                                                                                                                                                                                                                                                              P.;
surface
                                                                                                                                                                                                                                              141 AQKAEETKEKAGEY - - - - - KNYTAQKAGEAKDTTLGKAGEYKDYAAQKA - - - - AEAKDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298 OKTGEYKDYSAQKAAETKDATMEKTKEYKDYTAQKAAETKDATMEKAKEAKDTTVQKTGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37 FKQYANDNGVDGEWTYDDATKTFTVTEKPEVIDASELTPAVTTYKLVINGKTLKGETTTK
                                              40 VEHKEEVSGGPG-----VIGSILKSVQGTLGQAK-----EVVVGKAHDTAE-VSRENT
                                                                                                                                                                                                                                                                                               179 TAEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPE--EPKEEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RFAGKKVDEKPEEPMDTYKLIL-NGKTLKGETTTEAVDA--ATAEKV------
                                                                                                                                                                                                                                                                                                                                                                                               237 TIKANLIYADGK----TQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   676-682; 938-948; 1156-1168; 1176-1185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hilden P., Savolainen K., Tyynelae J., Vuento M., Kuusela "Purification and characterisation of a plasmin-sensitive protein of Staphylococcus aureus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P80544; 092F62;
01-FEB-1996 (Rel. 33, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MRA-2002 (Rel. 41, Last annotation update)
Methicillin-resistant surface protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1637 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   397 AVD------AETAEKAFKQY 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               402 AMDMFLGKKEEVKGKAGETAEAAKEKY 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eur. J. Biochem. 236:904-910(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96270743; PubMed=8665912;
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STRAIN=168;
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                                 Pero
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 17;
         Pfam; PF00746; Gram_pos_anchor; 1.
PROSITE; PS00343; GRAM_POS_ANCHORING; FALSE_NEG.
Cell wall; Transmembrane; Antibiotic resistance; Glycoprotein; Repeat;
                                                   POTENTIAL.

METHICILLIN-RESISTANT SURFACE PROTEIN.
141 X ANDEM REPEATS OF D-[SAG].
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                                                                                                                              346
                                                                                                                                                                                       87 EQVDVTKDTTEQASTEE---KAN----TTEQASTEEKADTTEQATTEEAPKAEG- 133
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                                                                                                                                                                                                                                ---TDKVETEEAPKAEETDKAT-----TEEAPKAEETDKATEEAP 170
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                                                                                                                                                                                                                                                                                                                                                                                                  361
                                                                                                                                                                                                                                                                                                                                                                                                                      347 DGEWTYDDATKTFTVTEKPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETAEK- 405
                                                                                                                                                                                                                                                                                                                                                                                                                                          QPRATFRSVSSNARTTNVNYSATALRAAAQDTVTKKGTGNFTAHGDIIHKTYKEEFPNEG 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1990 (Rel. 15, Created)
01-FBE1996 (Rel. 31, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Bacillopeptidase F precursor (EC 3.4.21.-) (Esterase) (RP-I protease)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sloma A., Rufo G.A. Jr., Rudolph C.F., Sullivan B.J., Theriault K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Bacillopeptidase F of Bacillus subtilis: purification of the protein
                                                                                                                                                Gaps
                                                                                                                                                                   62
                                                                                                                                                                   ENKEETPETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGE
                                                                                                                                                                                                             63 YTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAY
                                                                                                                                                                                                                                                    123 RYADALKKDNGEYTVDVADKGYTLNIKFA---GKEKTPEEPKEEVTIKANLIYA----D
                                                                                                                                                                                                                                                                        171 K------TEETDKATTEEAPAAEETSKAATEEAPKAEETSKAATEEAPKAEET
                                                                                                                                                                                                                                                                                            175 GKTQTAEFKGTFEE---ATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEE
                                                                                                                                                                                                                                                                                                                218 EKTATEEAPKTEETDKVETEEAPK----AEETSKAATEKAPKAEETN----KVETEEA
                                                                                                                                                                                                                                                                                                                                      PKEEVTIKANLIYADGKTQTAEFKGTFAEATA - - - - EAYRYADLLAKENGKYTADLEDG
                                                                                                                                                                                                                                                                                                                                                  GYTINIRFAGKKVDEKPEEPMDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYANDNGV
                                                                                                                                                                                                                                                                                                                                                                                          Indels 109;
                                                                                                                           Length 1637;
                                                                                                      75BE9ADB469BD309 CRC64;
                                                                                                                                     ; Pred. No. 0.46;
34; Mismatches 200;
                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A., AND SEQUENCE OF 195-222.
MEDLINE-90170864; Pubmed-2106512;
MEDLINE-90170864. Pubmed-2106512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1433 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---AFKQYANDN-GVDGVWTYDDA---TKTFTVT 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 422 TLTAFNTNFNPNTGTKGALEYNDKIDFNKDFTIT 455
                                                                                                                          Query Match 6.8%; Score 151.5; Best Local Similarity 24.4%; Pred. No. 0.4 Matches 111; Conservative 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=1423;
                                                                                             PROTEINS
InterPro; IPR001899; Gram_pos_anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cloning of the gene.";
Bacteriol. 172:1470-1477(1990)
                                                                                                        MM.
                                                                                                      1637 AA; 174573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (90 kDa serine proteinase).
BPR OR BPF.
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1637
1582
1603
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49
1301
1598
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01-FEB-1996 (
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ID SUBF_BACSU
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REVISIONS.
                                                                                                       SEQUENCE
                                                                       DOMAIN
                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pero J.
                                          Signal
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                                                              CHAIN
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                              Sullivan B.J., Theriault K.A.,
                                                                                                                                                                                                         Wu X.-C., Nathoo S., Pang A.S.-H., Carne T., Wang S.-L.; "Cloning, genetic organization, and characterization of a structural gene encoding bacillopeptidase From Bacillus subtilis."; J. Biol. Chem. 265:6845-6850(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kato T., Yamagata Y., Arai T., Ichishima E.;
"Purification of a new extracellular 90-kDa serine proteinase with isoelectric point of 3.9 from Bacillus subtilis (natto) and elucidation of its distinct mode of action.";
Biosci. Biotechnol. Biochem. 56:1166-1168(1992).
-: SUBCELLULAR LOCATION: Secreted.
-: SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Masuda E.S., Anaguchi H., Sato T., Takeuchi M., Kobayashi Y.; "Nucleotide sequence of the sporulation gene spoilGA from Bacillus subtilis.";
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SIMILARITY).
SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                         Beall B., Lowe M., Lutkenhaus J.; "Cloning and characterization of Bacillus subtilis homologs of Escherichia coli cell division genes ftsZ and ftsA."; J. Bacteriol. 170:4855-4864(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHARGE RELAY SYSTEM (BY
CHARGE RELAY SYSTEM (BY
CHARGE RELAY SYSTEM (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase; Serine protease; Zymogen; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Subtilist; BG10233; bpr.
InterPro; IPR000209; Peptidase_S8.
Pfam; PF00082; Peptidase_S8; 1.
PROFFA; SUBTILISIN.
PROSITE; PS00136; SUBTILASE_ASP; FALSE_NEG.
PROSITE; PS00136; SUBTILASE_HIS; 1.
PROSITE; PS00138; SUBTILASE_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                           Sloma A., Rufo G.A. Jr., Rudolph C.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic Acids Res. 18:657-657(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1410-1433 FROM N.A. STRAIN=168 / MARBURG; MEDLINE=90174995; PubMed=2106671;
                                                                                     Bacteriol. 172:5520-5521(1990)
                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=90216713; Pubmed=2108961;
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-211 FROM N.A. MEDLINE=89008108; PubMed=3139638;
MEDLINE=90368623; PubMed=2118514;
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EMBL; J05400; AAA83362.1; -.
EMBL; M22630; AAA22458.1; -.
EMBL; A1744; CAA35224.1; -.
EMBL; 299111; CAB13403.1; -.
EMBL; Z99112; CAB13404.1; -.
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A36734; A36734.
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MEROPS; S08.017
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        27;
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                                                                                                                                                                                                                                                                                                                                         61 GEYTVDVADKGYTLNIKFAGKEKTPE-EPKEEVTIKANLIYADGKTQTAEFKGTFEEAT- 118
                                                                                                                                                                                                                     Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
T -> A (IN REF. 6).

A -> V (IN REF. 3).

KHOMA -> N (IN REF. 3). . .

QPQVLP -> RTRLYS (IN REF. 3).

AQVSVVETG -> FCRSRHKSV (IN REF. 3).
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01-MAY-1991 (Rel. 18, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
Endothelial actin-binding protein (ABP-280) (Nonmuscle filamin)
FLNI OR FLN.
                                                                                                                                                                                                                59; Mismatches 187; Indels 176;
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MEDLINE-905361737; PubMed=2391361;
GOLIIn J.B., Yamin R., Egan S., Stewart M., Stossel T.P.,
Kwiatkowski D.J., Hartwig J.H.;
"Human endothelial actin-binding protein (ABP-280, nonmuscle
filamin): a molecular leaf spring-";
J. Cell Biol. 11:1089-1105(1990).
                                                                                                                                                                      Score 149; DB 1; Length 1433;
Pred. No. 0.54;
                                                                                                         33 MISSING (IN REF. 3).
154577 MW; 98DF6846897807C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----IKANLIYADGKTOTA------
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                                                                                                                                                                         6.7%; Score 149;
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143 AA;
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SEQUENCE FROM N.A.
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P21333;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                           *Mapping of two genes encoding isoforms of the actin binding protein ABP-280, a dystrophin like protein, to Xq28 and to chromosome 7."; Hum. Mol. Genet. 2:761-766(1993).

-1- FUNCTION: PROMOTES ORTHOGONAL BRANCHING OF ACTIN FILAMENTS AND LINKS ACTIN FILAMENTS TO MEMBRANE GLYCOPROFINS.

-1- SUBCLIDIAR LOCATION: PERIPHERAL CYTOPLASM.
-1- SUBCLIDIAR LOCATION: PERIPHERAL CYTOPLASM.
-1- TISSUE SPECIFICITY: UBIQUITOUS.
-1- PIM: PHOSPHORYLATION EXTENT CHANGES IN RESPONSE TO CELL ACTIVATION.
                                                                                                                                    "Long-range sequence analysis in Xq28: thirteen known and six candidate genes in 219.4 kb of high GC DNA between the RCP/GCP and
MEDLINE=96311563; PubMed=8733135;
Chen E.Y., Zollo M., Mazzarella R.A., Ciccodicola A., Chen C.-N.,
Zuo L., Heiner C., Burough F.W., Ripetto M., Schlessinger D.,
D'Urso M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DYSTROPHIN, FIMBRIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE FOUND IN
                                                                                                                                                                                                                                                                                                                                                  S., Rocchi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -:- SIMILARITY: THE ACTIN-BINDING DOMAIN IS OF A TYPE FOUNI ACTIN-BINDING PROTEINS (SUCH AS ACTININ, DYSTROPHIN, F. ARP-120, ABP-180, OR BETA-FOODIN).
-:- SIMILARITY: CONTAINS 2 CALFONIN-HOMOLOGY (CH) DOMAINS.
-:- SIMILARITY: CONTAINS 24 FILAMIN REPEATS.
                                                                                                                                                                                                                                                                                                             MEDIINE-93357748; PubMed-7689010;
Maestrini E., Patrosso C., Mancini M., Rivella S., Rocch.
Repetto M., Villa A., Frattini A., Zoppe M., Vezzoni P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTIN-BINDING (HEAD).
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PROSITE; PS00019; ACTININ_1; 1.
PROSITE; PS00020; ACTININ_2; 1.
PROSITE; PS50021; CH; 2.
PROSITE; PS50194; FILAMIN REPEAT; 24.
ACtin-binding; Phosphorylation; Repeat.
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InterPro; IPR001715; Calponin_hom
InterPro; IPR001298; Filamin.
                                                                                                                                                                                                                          Hum. Mol. Genet. 5:659-668(1996)
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EMBL, X44140; AAA92644.1; --
EMBL, X70082; CAA49687.1; --
EMBL, X70085; CAA49690.1; --
EMBL, X70085; CAA49690.1; --
HSSP; P13466; 1KSR.
MIM; 300017; --
                                                                                                                                                                                                                                                            [3]
SEQUENCE OF 1658-1772 FROM N.A.
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Pfam; PF00630; Filamin; 24.
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MEDLINE-95400292; PubMed-7670463;
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                    FROM N.A.
88C / AB972;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEAYAYADTLKKDNGEYTVDVADKG---YTLNIKFAGKEKTPEEP---KEEVTIKANLIY 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    818 AEADIDFDIIRNDNDTFTVKYTPRGAGSYTIMVLFA-DQATPTSPIRVKVEPSHDASKVK 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   877 AEGPGLSRTGVELGKPTHFTVNAKAAGKGKLDVQFSGLTKGDAVRDVDIIDHHDNTYTVK 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 ADGK------TQTAEFKG-----TFEEAT-AEAYRYADALKKDNGEYTVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    937 ----YTPVQQGPVGVNVTYGG-DPIPKSPFSVAVSPSLDLSKIKVSGLGEKVDVGKDQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 VTIKANLIYADGK -- TQTAEFKGTFEEATAEAYRYAD ---- LLAKENGKYTVDVADKGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217 TL-NIKFAGKEKTPEEPKEEVTIKANLIYADG------KTQTAEFKGTFAEA---TA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EAYRYADLLAKENGKYTADL-----EDGGYTINIRFAGKKVDEKPEEP-----MDTYKLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314 LNGKTLKGETTTEA----VDAATA--EKVFKQYANDNGVDGE---WTYDDATKT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----FTVTEK------PEVIDASELTPAVTTYKLVINGKTLKGE-----TTTKAVDAET
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2647;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Hypothetical 137.7 kDa protein in UGS1-FAB1 intergenic region.
YFR016C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              403 AEKA-----TYDDATKTFTVT 432
                                                                                                                                                                                                                                                                                              SELF-ASSOCIATION SITE, TAIL. CLEAVAGE (BY CALPAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                    6C1A07041DFA3D42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            b; Pred. No. 1.2;
66; Mismatches 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
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-> D (IN REF. 2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 148.5;
                              HINGE 1.
FILAMIN 16.
FILAMIN 17.
FILAMIN 18.
FILAMIN 19.
FILAMIN 20.
FILAMIN 21.
FILAMIN 22.
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FILAMIN 15
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Matches 116; Conservative
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1950
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P43597;
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PK-----EEVTIKANLIYADGKTQTAEFK 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKVDEKPEEPMDTYKLILN 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYAD-GKTQTAEFKGT---- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                525 AGEKSSIIEIEGSANSAKIS-------KDNLVLEDEAEAPTQENKPTEVVGE 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 --FEEATAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLI 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 YADGKTQTAEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEE 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               674 PKVVKRCTSGRPEDLQINERDPEVLKEDVRVPDEDVKPEIATTIENSEEDPKSORVQIS 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 GKTLKGETT------TEAVDAATAEKVF----KOYANDNGVDGEWTYDDATK 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATS--EAYAYADTLKKD 59
                                                                                                                         Sacchāromyces cerevisiae.";
Nat. Genet. 10:261-268(1995).
-!- SIMILARITY: SOME, TO MAMMALIAN NEUROFILAMENT TRIPLET M PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M., Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K., Yamazaki M., Tashiro H., Eki T., "Analysis of the nucleotide sequence of chromosome VI from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.6%; Score 148; DB 1; Length 1233;
21.2%; Pred. No. 0.51;
rative 64; Mismatches 181; Indels 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      358 TFTVTEKPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETAEK 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 protein.
1233 Aa; 137697 MW; C8A7CD2C6F0892F6 CRC64;
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01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Dextranse precursor (EC 3.2.1.11) (Alpha-1,6-glucan-6-glucanohydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             828 FIKVKAELENLDAPK--EAEVTAELNKENEDVEVDTEEDA-EVENSEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus downei (Streptococcus sobrinus).
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STRAIN=168;
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                         273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26;
                                                                STRAIN-6715 / UAB66;

MEDLINE-94292401; PubMed=8021165;

Wanda S.-Y., Curtiss R. III;

"Purification and characterization of Streptococcus sobrinus
dextranase produced in recombinant Escherichia coll and sequence
analysis of the dextranase gene.";

J. Bacteriol. 176:383-3860(1994).

-I- FUNCTION: MAY PLAY A ROLE IN SUCROSE-INDEPENDENT ADHERENCE TO THE
PELLICLE-COATED TOOTH SURFACE. THE ACTIVITY OF THIS ENZYME IS
OPTIMAL AT PH 5.3 AND AT 39 DEGREES CELSIUS.

-I- CATALYTIC ACTIVITY: Endohydrolysis of 1,6-alpha-D-glucosidic
                                                                                                                                                                                             MEMBRANE ANCHOR (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 TFEEATAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPE---EPKEEVTIKAN 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 DNGEYTVDV-ADK-----GYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----YKFSKHLK-----AGEGYKMQ---SGDLKIPASQFENNHGYLLKVR 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 LIYADGKTQTAEFKGTFEEATAEAY-RYA------DLLAKENGKYTVDVAD-KGYT 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 VRDADNNTLSEVNKAIAVESDWTKFPRYGIVGGSQDTNNSLLSKDADRYRAEIEKMKNMN 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --EATAEAYRYADLL 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 EQTP--PETSDASAPATTSADSVEKYAODATONOSSTSNGPGVIRATSAOVTATRSVVSS 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 EETPETPET-DSEEEVTIKANLI--FANGSTQ----TAEFKGTFEKATSEAYAYADTLKK 58
          Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 1337; .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 146.5; DB 1; Length 1337;
; Pred. No. 0.68;
64; Mismatches 181; Indels 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase; Glycosidase; Signal; Transmembrane; Repeat; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (BY SIMILARITY).
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                                                         31-36
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                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M96978; AAA21772.1; -.
InterPro; PR001899; Gram_pos_anchor.
Pfam: PF00746; Gram_pos_anchor; 1.
PR0SITE; PS00343; GRAM_POS_ANCHORING; 1.
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                                                        SEQUENCE FROM N.A., AND SEQUENCE OF STRAIN*6715 / UAB66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1337 AA; 143298 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.6%;
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Best Local Similarity 20.9<sup>3</sup>
Matches 110; Conservative
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1337
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                                  NCBI_TaxID=1317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1333
                       Streptococcus
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: THE REPEATED MOTIF IN THE C-TERMINUS HAS SOME SIMILARITY TO THE REPEAT IN E.COLI RHS GROUP OF PROTEINS (RHSA-D).
369 ILAE-NTNTGEAPVLPETEYAYNSDDRGYGAQGQPMSYTVKIPKDGQEEDVEIQRYYNPT 427
                                                                                        AKENGKYTAD-----LEDGGY-----TINIRFAGKKVDEKPEEPMDTYKLILNGKTLKG 321
                                                                                                                                                                                                                                                                                                                                      479 ---TEGYAEFLRAIKEKLPNYYLTVNDVNGEQIYRLKDGNQDVIYNEIWPFGPALPSEMA 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yoshida K.-I., Sano H., Seki S., Oda M., Fujimura M., Fujita Y.; "Cloning and sequencing of a 29 kb region of the Bacillus subtilis genome containing the hut and wapA loci."; Microbiology 141:337-343(1995).
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MEDLINE=97124196; PubMed=8969509;
Voshida K.1., Shindo K., Sano H., Seki S., Fujimura M., Yanai N.,
Miwa Y., Fujita Y.;
"Sequencing of a 65 kb region of the Bacillus subtilis genome
containing the lic and cel loci, and creation of a 177 kb contig
covering the gnt-sacXr region."
Microbiology 142:3113-3123(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular analysis of three major wall-associated proteins of
Bacillus subtilis 168: evidence for processing of the product of
gene encoding a 258 kDa precursor two-domain ligand-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED. MAY BE RELEASED INTO THE MEDIUM.
                                                                                                                                                                       428 SKLWQDYIADKMGQAMKNGGFDGWQGDTIGDNEVYSYADKDSNDPSKKFWL-----
                                                                                                                                                                                                                                                                                                                                                                                                                              362 TEKPEVIDASELTPAVT -- TYKLVINGKTLKG-ETTTKAVDAETAE 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   536 AVKPNTVTSRPVLTKVRQGDWKISIVGAYMEGSENGGSKADAEAGK 581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0cT-1994 (Rel. 30, Created)
01-0cT-1994 (Rel. 30, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2334 AA
                                                                                                                                                                                                                                                           322 ETTTEAVD --- AATAEKVFKOYANDNGVDGE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wall-associated protein precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93302506; PubMed=8316082;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1651 ---EKTTYTYDQADQLTNMTLSNGTSILHSYDKEGNEVSKTIRAGADQTYKFEYDVMGKL 1707
                                                                                                                            31 X 21 AA APPROXIMATE TANDEM REPEATS OF X(4)-G-X(4)-[YF]-X-D-X(2)-G-X(4).
                                                                                                                                                                                                                                                                                                                                                                                                                                  71 GYTLNIKF------AGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 TFEEATAEAYRYADAL-------KKDNGEYTVDV---ADKGYTLNIKFAGKE 154
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                                                                     OR 32 (POTENTIAL).
WALL-ASSOCIATED PROTEIN.
3 X 101 AA APPROXIMATE TANDEM REPEATS.
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ive 70; Mismatches 214; Indels 156;
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or send an email to license@isb-sib.ch)
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           EMBL; L05634; AAA22883.1; -. EMBL; D31856; BAA06656.1; -. EMBL; D29985; BAA06260.1; -. EMBL; D3026; BAA11683.1; -. EMBL; 299124; CAB15959.1; -.
                                              PIR; S32920; S32920.
Subtilist; BG10797; wapA.
InterPro; IPR003305; CBD_6.
Pfam; PF02018; CBD_6; 1.
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Matches 118; Conservative
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2334 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE OF AXONAL CALIBER.

PTH: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE CEPTELS OF PHOSPHORYLATION BEING ALTERED DEVELOMENTALLY AND COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.

SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                   1827 NQFTYNKLDQMIEMKDSTSSYSFDYDENGNVQTFITGNGGGTSFSYDERNLVSSLHIGDK 1886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2004 AVTKKGE------DKPFATYKYDEKGNRIQKTVNGKVTNYFYDGDSLNVLYETDA-DNN 2055
                                                                                  NGNETSVVNKEQNTTKKRTFDNKNRLTELTDRGGSQTWTYPSDSDKLKTFSWIHGDQKGT 1826
                                                                                                                                                                                                                                                                                                                                                                                                                                            NGGDILTESYEYDANGNRTTINSSASGKVQYEYGKLNQLVKETHEDGTVIEYTYDGFGNR 1946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KTV----TTIKDGSSKTVNASFNIMNQLTKVNDESISYDKNGNRTSDGKFTYTWDAEDNLT 2003
---EPKEEVTIKA-NLIYADGK-- 248
                                                                                                                                                                        -----TQTAEFKGTFAE------E 275
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                                                                                                                                                                                                                                                                                                                                            NG-----KYTADLEDGGYTINIRFAGK-----KVDEKPEEPMD-----TYKLILNG 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KTLKGETTTEAVDAATAEKVFK----QYANDNGV------DGEWTYD-DATKTFT
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Julien J.-P., Meyer D., Flavell D., Hurst J., Grosveld F.; "Cloning and developmental expression of the murine neurofilament
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
M protein (160 kDa neurofilament protein)
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MEDLINE=87158637; PubMed=3103856;
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P08553; O61961;
O1-AUG-1988 (Rel. 08, Created)
01-NOV-1990 (Rel. 16, Last sequ
16-OCT-2001 (Rel. 40, Last ann
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NCBI_TaxID=1392;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                574 AEAKEEKKIEGK----VEEVAVKEEIKVEKPEKAKSPMPKSPVEEVKPKPEAKAGKGEQK 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 TAE-FKGTFEEATAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 IKANLIYADGKTQTAEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGK 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EKTPEE-PKEEVTIKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLE 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DGGYTINIRFAGKKVDEKPEEPMDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYANDN 344
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01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
S-layer protein sap precursor (Surface layer protein) (Surface array
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    518 KEEEEEGQEEEEEEDEGVKSDQAEEGGS----EKEGSSEKDEGEQEEEGETEAEGEGEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         630 EEEKVEEEKKEVTKESPKEEKVEKKE--EKPKDVADK------KKAESPVKEKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --------VSPAEEKKGEDSSDDKVVV-------TKKVEKITSE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.4%; Score 143.5; DB 1; Length 848; 22.9%; Pred. No. 0.57; Live 53; Mismatches 151; Indels 103;
                                                                                                                                                                                                                                                                                                                                                                 COIL 2B.
O-LINKED (GLCNAC) (BY SIMILARITY).
                                                                                    InterPro; IPR001664; IF.
Pfam; PF00038; filament; 1.
PROSITE; PS00226; IF; 1.
Intermediate filament; Coiled coil; Neurone; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 -> RR (IN REF. 2).
5F251F274D0F13B6 CRC64;
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Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                              2)
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S -> F (IN REF.
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LINKER 2.
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COIL 1A.
                                                                                                                                                                                                                                                                                            COIL 1B.
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             EMBL; X05640; CAA29127.1; -. EMBL; M20481; AAA39815.1; -. PIR: S00030; S00030. MGD; MGI:97314; Nfm.
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247
264
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430
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848 AA;
                                                                                                                                                                  Glycoprotein.
INIT_MET
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P49051;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29;
                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250 DKVLVKEVTLSEDKKSATVELYSNLAAKQTYTVDVNKVGKTEVAVGSLEAKTIEMADQTV 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YADGKTQ---TAEFKGTFEEATAEAYRY-ADALKKDNGEYTVDVADKGYTLNIKFAGKE- 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            369 GKVVAESK-EVKVSAEGAAVASISNWTVAEQNKADFTSKDFKONNKVYEGDNAYVQVELK 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DQFNAVTTGKVEYESLNTEVAVVDKATGKVTVLSAGKAPVKVTVKDSKGKELVSKTVEIE 487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258 FAEAT------AEAYRYADLLAKENG----KYTADLE---DGGYT-INIRFAGK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                      AVENKEETPETPETDSEEEVTIKANLIFANGSTQTAE--FKGTFEKATSEAYAYAD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----TLKKDNGEYTVDV----ADKGYTLNIKFAGKEKTPEEPKEEVTIKA--NLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .84 GTFEEATAEAYRYADL-----LAKENGKYTVDVADKG-YTLNIKFA-GKE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 814;
                                                                                                                                                                                                                                                                                    -!- PTM: PROBABLY GLYCOSYLATED.
-!- SIMILARITY: CONTAINS 3 S-LAYER HOMOLOGY (SLH) DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Repeat; Cell wall; S-layer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.4%; Score 142.5; DB 1;
22.5%; Pred. No. 0.62;
iive 59; Mismatches 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S-LAYER PROTEIN SAP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; 236946; CAA85408.1; -. InterPro; IPR003343; Big_2. InterPro; IPR001119; SLH. Pfam; PF02368; Big_2; 1. Pfam; PF00395; SLH; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Matches 129; Conserv
                                                   STRAIN-STERNE;
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send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                            430
                                                                                                                                    Glycoprotein.
INIT_MET
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Biol. Chem. 268:16679-16687(1993).

-1- FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M, AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.
-1- PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, NFM IS PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT IS THOUGHT THAT PHOSPHORYLATION OF NFH RESULTS IN THE FORMATION OF INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OF AXONAL CALIBER.

PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING
OF THE LARGER NEROFFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE
LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND
COINCIDENT WITH A CHANGE IN THE NEUROFILLAMENT FUNCTION.
                           -----DATDAQVTVQNNSVITVGQGAKAGETYKVTVVLDGKLITTHSFKVVDTAPTA 708
                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIINE-92332596; Pubmed-1321159;
Kelly B.M., Gillespie C.S., Sherman D.L., Brophy P.J.;
"Schwann cells of the myelin-forming phenotype-express neurofilament
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Glycosylation of mammalian neurofilaments. Localization of multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-93346421; PubMed-8344946;
Dong D.L.-Y., Xu Z.-S., Chevrier M.R., Cotter R.J., Cleveland D.W.,
Hart G.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O-linked N-acetylglucosamine moieties on neurofilament polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                      rat NF-M,
 LL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92165797; PubMed=1537832; Xu Z.-S., Liu W.-S., Willard M.B.; "Identification of six phosphorylation sites in the COOH-terminal tail region of the rat neurofilament protein M.";
                                                                                                                                                                                    01-0CT-1989 (Rel. 12, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Neurofilament triplet M protein (160 kDa neurofilament protein)
(Neurofilament medium polypeptide) (NF-M).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY
346 VDGEWTYDDATKTFTVTEKPEVIDASELTPAVTTYK--LVINGKTLKGET---
                                                                                                                                                                                                                                                                                                                                                                                    Napolitano E.W., Chin S.S.M., Colman D.R., Liem R.K.H.; "Complete amino acid sequence and in vitro expression of the middle molecular weight neurofilament protein."; J. Neurosci. 7:2590-2599(1987).
                                                                                                                                                                845 AA
                                                          ------NDNGVDGV 419
                                                                                   709 KGLAVEFTSTSLKEVAPNADLKAALLNILSVDGV 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION SITES, AND REVISION TO 500.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Biol. Chem. 267:4467-4471(1992).
                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=87282618; PubMed=2441012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell Biol. 118:397-410(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYDRATE-LINKAGE SITES.
                                                                                                                                                                STANDARD;
                                                          KAVDAETAEKAFKOYA---
                                                                                                                                                                                                                                                                     NEF3 OR NEFM OR NFM.
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
                                                                                                                                                             NFM_RAT
P12839; Q63370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-WISTAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      631 KVEEKKEVAKESPKEEKVEKKE--EKPKDVPDK-------KKAESPVKEKAVE-E 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170 LIYADGKTQTAEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTP 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EE-PKEEVTIKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGY 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   289 TINIRFAGKKVDEKPEEPMDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVDG 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QESKKEDIAINGEVEGKEEEEQETQEKGSGQE------EEKGVVTNGLD---
                                              InterPro; IPR001664; IF.
Pfam; PF00038; filament; 1.
PROSITE; PS00226; IF; 1.
Intermediate filament; Coiled coil; Neurone; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MISSING (IN REF. 1).
316C41655B11197D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.3%; Score 141.5; DB 1;
23.4%; Pred. No. 0.73;
ve 51; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R -> P (IN REF. 2).
V -> L (IN REF. 2).
                                                                                                                                                                                                                                                                                                                    /FIIG-CAR_000130.
0-LINED (GLCNAC).
/FIIG-CAR_000131.
PHOSPHORYLATION.
PHOSPHORYLATION.
PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                     O-LINKED (GLCNAC)
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PHOSPHORYLATION.
MISSING (IN REF.
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                                                                                                                            BY SIMILARITY. HEAD.
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                                                                                                                                                                                                                                                                      LINKER 2.
                                                                                                                                                                                                          LINKER 1.
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                                                                                                                                                                                                                                                                                                                                                          Local Similarity 23.4%; es 92; Conservative 5
EMBL; M18628; AAA41696.1;
EMBL; Z12152; CAA78136.1;
GlycoSuiteDB; P12839; -.
                                                                                                                                                                                                        147
246
263
285
285
410
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31 13:39:58 2002

Thu Oct

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MEDLINE=97405699; PubMed=9260743;
MEDLINE=97405699; PubMed=9260743;
MEDLINE=97405699; PubMed=9260743;
MEDLINE=97405699; PubMed=9260743;
MEDLINE=97405699; PubMed=9260743;
MEDLINE=97405699; PubMed=9260743;
MEDLINE PROBLEM OF MICHOLOUSE MAPIBOR (MAPIB)

In rat CNS and PNS during development.",
J. Neurosci. Res 49:319-332(1997).

I. FUNCTION: The function of brain MAPS is essentially unknown.
Phosphorylated MAPIB may play a role in the cytoskeletal changes that accompany neurite extension. Possibly MAPIB Binds to at least two tubulins neubmits in the polymer, and this bridging of subunits might be involved in nucleating microtubule polymerization and in stabilizing microtubules.

II SUBURITY: 3 different light chains, LCl, LC2 and LC3, can associate with MAPIA and MAPIB proteins.

Cerebellum and cerebrum). Not expressed in liver, spleen, kidney,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nerve levels are high early in development but decrease during postnatal development and are low in adults. In dorsal root ganglia levels remain high throughout development.

INDUCTION: By nerve growth factor.

DOMAIN: Has a highly basic region with many copies of the sequence KKEE and KKEI/V, repeated but not at fixed intervals, which is responsible for the binding of MAPIB to microtubules.

PTM: LC1 is coexpressed with MAPIB. It is a polypeptide generated from MAPIB by protecolytic processing. It is free to associate with both MAPIB and MAPIB. It interacts with the amino-terminal region of MAPIB (By similarity).
                 01.APR-1990 (Rel. 14, Created)
16-007-2001 (Rel. 40, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
Microtubule-associated protein 1B (MAP 1B) (Neuraxin) [Contains: MAP1
                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEVELOPMENTAL STAGE: In cerebral cortex, spinal cord and sciatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Electic A., Grenningloh G., Hermans-Borgmeyer I., Kirsch J., Littauer U.Z., Prior P., Gundelfinger E.D., Schmitt B., Betz H.; "Neuraxin, a novel putative structural protein of the rat central aervous system that is immunologically related to microtubule-associated protein 5."; EMBO J. 8:2879-2888(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAUTION: A C-terminal fragment of this protein (residues 1597 2459) was originally described as neuraxin in ref.3.
                                                                                                                                                                                                                                                                                                                                           end of the rat microtubule-
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domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1541-2459 FROM N.A., AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-SPRAGUE-DAWLEY; TISSUE-Brain, and Glial tumor; MEDILINE-92347314; PUBMed-1659092; Zauner W., Kratz J., Staunton J., Feick P., Wiche G.; Identification of two distinct microtubule binding d
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 96-2459 FROM N.A., DOMAIN, AND INDUCTION
                                                                                                                                                                                                                                                      SEQUENCE OF 1-142 FROM N.A.

STAINA-SPRAGUE-DANLEY; TISSUE-TESTIS;

MEDLINE-96257242; PubMed-8666295;

Liu D., Fischer I.;

Isolation and sequencing of the 5' end or
associated protein (MAPIB)-encoding CDNA.

Gene 172:307-308(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eur. J. Cell Biol. 57:66-74(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Spinal cord;
MEDLINE=90059871; Pubmed=2555150;
Q9ER21; Q9QW92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: TO MAP1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       recombinant rat MAP 1B."
                                                                                                                                                 Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTM: Phosphorylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     heart or muscle.
                                                                                                      light chain LC1]. MAP1B.
                                                                                                                                                                                                           NCBI_TaxID=10116;
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
 EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1698 EEPSYTQDNDLSELISV--SQVEASPSTSSAHTPSQIASPLQE-----DTLSDVVPPRDM 1750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1751 SLYASLASEKVQSLE----GEKLSPKSDISPLTPRESSPTYSPGFSDSTSGAKESTAAYQ 1806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1807 TSSSPPIDAAAAEPYGFRSSMLFDTMQHHLALSRDLTTSSVEKDNGGKTPGDFNYAYQKP 1866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1918 -EKTTKTPEDGGYSCEI----TEKTTRTPEEGGYSYEISEKT-----TRTPEVSGYT 1964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIK-ANLIYADG-------KTQTAEFK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 GT----FEEATAEAYRYAD-----ALKKDNGEYTVDVADKGYT---LNIKFAGK 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                CONTAINS MANY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259 AEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKVDEK----PEEPMDTYKLIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1965 YEKTERSRRLLDDIS--NG--YDDTEDGGHTLGDCSYSYETTEKITSFPES--ESYSYET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96;
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the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MW; 2E3F6872DEDB8BA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                               (HIGHLY BASIC, CO
                                                                                                                                                                                                   MAP1 LIGHT CHAIN LC1
                                                                                                                                                                                                                                                                                                                                                                                                     M -> V (IN REF. 1).
T -> S (IN REF. 1).
R -> K (IN REF. 3).
L -> I (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59; Mismatches
                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.3%; Score 141;
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KKEE AND P
LYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.
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GLU-RICH.
                                                                                                                                                                                                             MAPIB 1.
MAPIB 2.
MAPIB 3.
MAPIB 4.
MAPIB 5.
MAPIB 6.
MAPIB 6.
MAPIB 7.
                                                                                                                                                                                     Phosphorylation
                                                                                                                  EMBL; X16623; CAA34620.1; ALT_SEQ.
PIR; S06017; S06017.
InterPro; IPR000102; MAP1B_neuraxin.
                                                                                                                                                          Pfam; PF00414; MAP1B_neuraxin; 10.
PROSITE; PS00230; MAP1B_NEURAXIN; 8.
                                                                                          EMBL; U52950; AAB17068.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.48;
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Search completed: October 29, 2002, 09:30:03 Job time: 19.571 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

October 29, 2002, 09:27:36 ; Search time 18.2057 Seconds (without alignments) 2290.646 Million cell updates/sec Run on:

US-08-325-278B-3
2235
1 AVENKEETPETPETDSEEEV......GVDGVWTYDDATKTFTVTEM 434 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	immunoglobulin-bin	Iq liqht chain-bin	protein L precurso	protein G precurso	streptococcal surf	IgG-binding protei	plasma protein rec	collagen adhesin -	late embryogenesis	late embryogenesis	Ig light chain-bin	late embryogenesis '	neurofilament prot	immunoglobulin Al	hypothetical prote	fibrinogen-binding	neurofilament medi	choline binding pr	neurofilament trip	embryonic protein) - sea lampr	EF protein - Strep	lactoferrin-bindin	probable peptidogl	surface protein pr	hypothetical prote	cyst germination s	hypothetical prote	ratio [coooding of
0	Descr	immuni	Iq lic	prote	prote	strep	īd-psī	plasma	collac	late	late	oil el	late	neuro	immun	hypot	fibrin	neuro	cholir	neuro	embryo	NF-180 -	EF pro	lacto	probal	surfac	hypotl	cyst	hypot	an oud
SUMMAKIES	ID	A45063	A42808	S54396	S00128	S42574	A24496	S55890	A42404	T47561	H84782	A34483	JC6171	T52485	C95008	B98047	T28680	150479	Н98120	A27864	S04909	151116	S33441	H81070	AB1347	T30944	T18674	T31108	T34418	F95013
	DB	7	7	~	7	7	~	7	~	7	7	7	7	7	7	7	7	7	~	~	7	~	~	~	7	7	7	~	7	^
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æ	Query Match	100.0	71.0	56.5	31.7	31.6	30.6	18.1	8.4	8.1	7.8	7.7	7.5	7.2	7.1	7.1	7.0	7.0	7.0	7.0	6.9	6.9	6.9	6.9	6.9	6.9	9.8	6.7	6.7	6.7
	Score	2235	1587.5	1263.5	708	706.5	683	404	188.5	182	175	171.5	168	162	159	159	157.5	157	156.5	156	155	154.5	154.5	154	154	153.5	152	150	150	149.5
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9 Οy qq

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AF1772	A36734	E97944	H88733	A37098	S56271	S61441	AD1525	T14850	T25697	T29757	B33856	G41662	T30291	C84346	AF1450
7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
938	1433	1876	066	2647	1233	2508	657	1099	1229	6642	745	891	1337	1363	1993
6.7	6.7	6.7	9.9	9.9	9.9	9.9	9.9	9.9	9.9	9.9	9.9	9.9	9.9	9.9	9.9
149.5	149	149	148.5	148.5	148	148	147.5	147.5	147.5	147.5	147	147	146.5	146.5	146.5
30	31	32	33	34	32	36	37	38	36	40	41	42	43	44	45

ALIGNMENTS

roperties.	;0							
999) 1999)	S.	60	120	180	240	300	360	420
RESULT 1 A45063 immunoglobulin-binding protein LG - Peptostreptococcus magnus c;Speciaes: Peptostreptococcus magnus c;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 15-Oct-1999 C;Accession: A45063 E;Kihlbergy B.M.; Sjobzing, U; Kastern, W.; Bjorck, L. J. Biol. Chem. 267, 25583-25589, 1992 A;Title: Protein LG: a hybrid molecule with unique immunoglobulin binding properties. A;Title: Protein LG: a hybrid molecule with unique immunoglobulin binding properties. A;Tecession: A45063; MUID:93094283 A;Scatus: preliminary A;Accession: A45063 A;Scatus: preliminary A;Molecule type: mRNN; protein A;Residues: 1-455 <kih> A;CNSS-references: GB:S50809; NID:g261705; PIDN:AAA03280.1; PID:g261706 A;Cnoss-reference extracted from NCBI backbone (NCBIN:120302, NCBIP:120303)</kih>	Ouery Match 100.0%; Score 2235; DB 2; Length 455; Best Local Similarity 100.0%; Pred. No. 1.9e-110; Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps	AVENKEETPETPETDSEEEVIIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDN 	GEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGFFEEATAE 	AYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTA 	EFKGTFEEATAEATRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKA 	NLIYADGKTQTAEFKGTFAEATAEAYRYADLIAKENCKYTADLEDGGYTINIRFAGKKVD 	EKPEBPMDTYKLILNGKTLKGETTTBAVDAATAEKVFKQYANDNGVDGEWTYDDATKTFT 	VTEKPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKOYANDNGVDGYW
LT 1 63 mogld nogld nogld eccles cess hilber ferencess at us lecul sidue oss-tes:	ery l st Lk tche	1 22	61	121	181	241	301	361
RESULT A45063 immunoc C;Spec; C;Date C;Acces C;Acces A;Title A;Title A;Acces A;State A;Molec A;Molec A;Cross A	Qu Be Ma	Qy Db	Qy Db	Qy Db	Oy Db	Qy Db	Qy	Qy

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Conservative
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Best Local $
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Matches
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       Ny Alternate names: protein L
C. Species: Peptostreptococcus magnus
C. Accession: A421804 * Resquence_revision 19-May-1994 * text_change 07-May-1999
C. Accession: A42808 * A41493
E. Kastern, W.: Sjoebring, U.: Bjoerck, L.
J. Biol. Chem. 267, 12820-12825, 1992
A. Tille: Structure of peptostreptococcal protein L and identification of a repeated immu A; Reference number: A42808 * MUID: 92316971
A. Tille: Structure of peptostreptococcal protein L and identification of a repeated immu A; Reference number: A42808 * MUID: 92316971
A. Status: preliminary
A. Molecule type: DNA
A. Restern, W.: Holst, E.: Nielsen, E.: Sjoebring, U.: Bjoerck, L.
Infect. Immun. 58, 1217-1222, 1990
A. Tille: Protein L, a bacterial immunoglobulin-binding protein and possible virulence de A; Reference number: A41493; MUID: 90215984
A. Status: preliminary
A. Molecule type: DNA
A. Residues: 202-275 < KAZ>
C. Keywords: immunoglobulin
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C; Species: Peptostreptococcus magnus
A; Variaty, Strain 3316
C; Date: 27-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 15-Oct-1999
C; Accession: S54396
R; Murphy, J.P.; Duggleby, C.J.; Atkinson, M.A.; Trowern, A.R.; Atkinson, T.; Goward,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 VENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKAN 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            275 FKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKAN 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKVDE 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      357
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395 KPEBKEQVTIKENIYFEDGTVQTATFKGTFABATA=-RYADLLSKEHGKYTADLEDG 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        358 TFTVT------EKPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETAE 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KPEEPMD-TYK--LILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVD-GEWTYDDATK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        light chain-binding protein precursor - Peptostreptococcus magnus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.0%; Score 1587.5; DB 2; Length 719; 76.3%; Pred. No. 3.2e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26;
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Matches 334; Conservative
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C; Species: Streptococcus sp.

A; Variety: Streptococcus sp.

A; Variety: Streptococcus sp.

A; Variety: Streptococcus sp.

C; Date: 30-Jun-1989 #text_change 19-May-2000
C; Accession: S00128; A27604; A26314

R; Olsson, A.; Eliasson, M.; Guss, B.; Nilsson, B.; Hellman, U.; Lindberg, M.; Uhlen, B; Olsson, A.; Eliasson, M.; Guss, B.; Nilsson, B.; Hellman, U.; Lindberg, M.; Uhlen, B; A; Reference number: S00128; MUID:88029445
A; Reference number: S00128; MUID:88029445
A; Reference number: S00128
A; Molecule type: DNA
A; Residues: 1-593 < CLS>
A; Note: the source is designated as Streptococcus G148
A; Note: the source is designated as Streptococcus G148
A; Note: the source is designated as Streptococcus G148
A; Note: part of this sequence, including the amino end of the mature protein, was con R; Sjoebring, U.; Falkenberg, C.; Nielsen, E.; Akerstroem, B.; Bjoerck, L.

A; Tille: Isolation and characterization of a 14-kDa albumin-binding fragment of strep A; Accession: A27604; MUID:88154455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: A27604
A;Molecule type: protein
A;Residues: 62-101 <530>
R;Guss, B.; Eliasson, M.; Olsson, A.; Uhlen, M.; Frej, A.K.; Jornvall, H.; Flock, J.I
EMBO J. 5, 1567-1575, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                             12;
Mol. Microbiol. 12, 911-920, 1994
A;Title: The functional units of a peptostreptococcal protein L.
A;Reference number: S54396; MUID:95020613
A;Accession: S54396
A;Status: preliminary; nucleic acid sequence not shown
A;Mollcule type: DNA
A;Residuaes: 1-992 < MUNA
A;Residuaes: 1-992 < MUNA
A;Residuaes: 1-992 < MUNA
A;Cross-references: EMBL:L04466; NID:9150673; PIDN:AAA67503.1; PID:9150674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 MERKLSEKETPE--PEEEVTIKANLIFADGSTQNAEFKGTFAKAVSDAYAYADALKKDNG 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQPGENPGITIDEWLLKNAKEEAIKELKEAGITSDLYFSLINKAKTVEGVEALKNEILKA 598
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                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 IKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 AEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKE--KTPEEPKEEVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                K-----VDE-----KPEEPM------DTY-KLILNGKTLKG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             599 HAGEETPELKDGYATYEEAEAAKEALKNDDVNNAYEIVQGADGRYYY--VLKIEVADEE
                                                                                                                                                                                                                                                                                                                                                                                                                     71;
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N;Alternate names: albumin-binding protein; cell wall-bound protein
                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                          56.5%; Score 1263.5; DB 2; Length
58.8%; Pred. No. 4.9e-59;
Live 36; Mismatches 90; Indels
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17;

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A;Title: The type-III Fc receptor from Streptococcus dysgalactiae is also an alpha(2) A;Reference number: S42574; MUID:94192673
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J. Bacteriol. 167, 870-880, 1986
J. Bacteriol. 167, 870-880, 1986
A;Title: Gene for an immunoglobulin-binding protein from a group.G Streptococcus
A;Title: Canabar: A24496; MUID:86304178
A;Accession: A24496
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-448 <FAHA
A;Residues: 1-448 <FAHA
A;Residues: L-48 <FAHA
A;Cross.references: GB:M13825; NID:g153822; PIDN:AAA03664.1; PID:g153823
A;Cross.references: GB:M13825; NID:g153822; PIDN:AAA03664.1; PID:g153823
A;Title: Streptococcal protein G. Gene structure and protein binding properties.
A;Reference number: A39041; MUID:91093154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Streptococcus sp.
C;Date: 17-Sep-1987 #sequence_revision 17-Sep-1987 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203 QAVQLEAPTVIDAPELTPALTTYKLVVKGNTF--SGETTTK----AIDTATAEKEFKQYA 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --GKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA--YRYA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DALKKDNGEYTVDVADKGYTLNIKFA---GKEKTPEEPKEEVTIKANLIYADGKTQTAEF 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TFTVTEKPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVD 417
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                      A;Cross-references: EMBL:Z29666; NID:g470220; PIDN:CAA82764.1; PID:g470221
C;Superfamily: M5 protein
                                                                                                                                                                                                                                                                                                                                                                                                   24 ANLIFANGSTQTAEFKGTFEKATSEAYAYADTLK-KDNGEYTVDVADKGYTL--NIKFA- 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 KGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFA---GKEKTPEEPKEEVTIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240 ANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 DEKPE--EPMDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATK
                                                                                                                                                                                                                                                                          Length 664;
                                                                                                                                                                                                                                                                             31.6%; Score 706.5; DB 2;
43.9%; Pred. No. 5.2e-30;
tive 51; Mismatches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IgG-binding protein - Streptococcus sp. (group G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein
A; Residues: 34-42,'N',45-48;62-76;186-200 <SJO>
                                                                                                                                                                                                                                                                                                                                     51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVWTYDDATKTFTVTEM 434
                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                            A; Molecule type: DNA
A; Residues: 1-664 <JON>
                                                                                                A; Status: preliminary
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                                                                    A; Accession: S42574
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                                                                                                                                                                                                                                                                                                                                        Matches 192;
                                                                                                                                                                                                                                                                                Query Match
Best Local 3
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C;Species: Streptococcus dysgalactiae
C;Species: Streptococcus dysgalactiae
C;Bate: 13-3an-1995 #sequence_revision 13-3an-1995 #text_change 19-May-2000
C;Accession: S4574
R;Jonsson, H.; Mueller, H.P.
Eur. J. Biochem. 220, 819-826, 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 LSDFLKSQTP-----AEDTVKSIELAEAKVLANRELDKYGVSDYHKNLINNAKTVEGVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 TPEEPKEEVTIKANLIYA-DG-----KTQTAEFKGTFEEATAEAYRYAD---LLAKENGK
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                                                                                                A;Molecule type: DNA
A;Residues: 114-593 <GUS>
A;Cross-references: GB:X04015; NID:g47071; PIDN:CAA27638.1; PID:g47072
C;Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;443-497/Region: C repeat
F;498-567/Domain: proline-rich <PRO>
F;568-593/Domain: carboxyl-terminal <CTD>
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Best Local Similarity 48.33
Matches 205; Conservative
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VTEM 498
                                                                 A; Accession: A26314
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Query Match 30.6%; Score 683; DB 2; Length 448; Best Local Similarity 53.2%; Pred. No. 5.46-29; Matches 176; Conservative 15; Mismatches 92; Indels 48; Gaps 9;	Qy 3
Ou 130 KONCEPTUONAANKOVAT MITERAACEERINDERINDERINTKAMI IVAACAMAARINDERINDERI 100	Dp 5
45 RNGGELTNILGNSETTLALRRESATADAVADAVAAAARNAGA	Qy 4
189 ATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKAN	Dp 3
Db 93 AAWEAAAADALAKAKADALKEFNKYGVSDYYKNLINNAKTVEGIKDLQAQVVESAKKAR 152	RESULT
OY 242 LIYA-DGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINI 292	collage
Db 153 ISBATDGLSDFLKSQTPAEDTVKSIELAEAKVLANRELDKYGVSDYHKNI 202	C;Speci C;Date:
QY 293 RFAGKKVDEKPEEPMDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYAND 343	C; Acces R; Patti
Db 203 INNAKTVEGVKELIDEILAALPKTDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYAND 262	A;Title
Qy 344 NGVDGEWTYDDATKTFTVTEKPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETA 403	A; Kerer A; Conte
Db 263 NGVDGEWIYDDATKIFIVTEKPEVIDASELIPAVITYKLVINGKTLKGETITKAVDAETA 322	A; Acces A; Statu
OY 404 EKAFKQYANDNGVDGVWTYDDATKTFTVTEM 434	A; MOLEC A; Resid A; Cross A; Note:
RESULT 7 S55890	Query Best Match
plasma protein receptor MAG precursor – Streptococcus dysgalactiae C;Species: Streptococcus dysgalactiae	^ 0
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 17-Mar-2000 C;Accession: S55890	. go
R;Jonsson, H.; Frykberg, L.; Rantamaeki, L.; Guss, B. Gene 143, 85-89, 1994	
A; Title: MAG, a novel plasma protein receptor from Streptococcus dysgalactiae. A; Reference number: S55890; MUID:94259307	Dp 2:
A;Accession: S55890 A;Status: preliminary A:Molecule trone: DNA	Qy
A. Residues: 1-413 < JON> A. Cross-reference: PMBE: 122708: NID: A75117: DIDN: AAA26021 1. DID: A475119	Db 6.
110,140,011, 11,142,020	0y 1:
Query Match 18.1%; Score 404; DB 2; Length 413; Rost Loral Similarity 32.3%; Dred No 2.2c-14.	o qa
les 141; Conservative 31	Qy 1
Qy 1 AVENKEETPETPETBSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYADTLKKDN 60	op 1
TVSPVTVATDA	Qy 2
61 GEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANL-IYADGKTQTAEFKGTFEEATA	
Db 67 LN-NLDIQEVLAKAGRDILASDSADTIKALLAEVTA 101	Qy 2.
QY 120 EAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQT 179	B qa
Db 102 EVTRLAFSELKD 132	0y 2
Oy 180 AEFKGTFEEATAEAYRADL-LAKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTI 238	o qu
IINDYTTKVENAKTAEDVKKIFEESQNI	Qy 3,
OY 239 KANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKK 298)6 qa
Db 187RIKTEKALKAAALAKAKADAIEILKKYGIGDYXI 220	Oy 4
299 VDEKPEEPMDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATKT	Db 10
Db 221ALINNGKTAEGVTALKD 237	

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jen adhesin - Staphylococcus aureus
sites: Staphylococcus aureus
s: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 10-Nov-1995
sssion: A42404; S27665
ii, J.M.; Jonsson, H.; Guss, B.; Switalski, L.M.; Wiberg, K.; Lindberg, M.; Hook
ii, J.M.; Johnsson, H.; Guss, B.; Switalski, L.M.; Wiberg, K.; Lindberg, M.; Hook
ii. Chem. 267, 4766-4772, 1992
le: Molecular characterization and expression of a gene encoding a Staphylococcu
srence number: A42404; MUID:92165839
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91 EVT-----TAEFKGTFEEATAEAY 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 SEA---YAYADTLKKDNG-------EYTVDVADKGYTLNIKFAGKEKTPEEPKE 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y Match 8.4%; Score 188.5; DB 2; Length 1185; Local Similarity 23.8%; Pred. No. 0.016; nes 136; Conservative 61; Mismatches 166; Indels 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : sequence extracted from NCBI backbone (NCBIP:83982)
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dues: 1-1185 <PAT>
s-references: EMBL:M81736
                                                                                                                                                                                                                                    us: preliminary
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ssion: A42404
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C.Species: Peptostreptococcus magnus
C.bate: 07-sep-1990 #sequence_revision 07-sep-1990 #text_change 16-Aug-1996
C.Accession: A34483
R.Akcrstroem, B.: Bjoerck, L.
J. Biol. Chem. 264, 19740-19746, 1989
A;Title: Protein L: an immunoglobulin light chain-binding bacterial protein. Characte A;Reference number: A34483; MUID:90062074
                                                                                                                                                                                                           20;
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    A;Molecule type: DNA
A;Residues: 1-448 <STO>
A;Cross-references: GB:AE002093; NID:g4415909; PIDN:AAD20140.1; GSPDB:GN00139
C;Genetics:
                                                                                                                                                                                                                                                                                      79 EAAESTKEGAQIASEKAVGAK-------DATVEKAKET----ADYTAEKVGE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 YTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAY 122
                                                                                                                                                                                                                                                                                                                                                                                                                               123 RYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEF 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 KGTFEEATAE------AYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPE 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---EPKEEV--TIKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLED 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        286 GGYTINIRFAGKKVDEKPEEPMDTYKLILNGKTLKGETTTEAVDAAT-----AEKV 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              337 --FKQYANDNGVDGEWTYDDATKTFTVTEKPEVIDASEL------TPAVTTYKL 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205 VGEYKDYTVDKAVEARDYTAEKAIEAKDKTAEKTGEY-----KDYTVEKATEGKDVTVS 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          348 EETKDSAAVRGNEAKGTIFGALGNVTEAIKSKLTMPSDIVEETRAAREHGGTGRTVVEVK 407
                                                                                                                                                                                                                                                     3 ENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig light chain-binding protein L - Peptostreptococcus magnus (fragments)
                                                                                                                                                                                                                                                                                                                                                                     259 KLGELKDSAVETAKRAMGFLSGKTEEAKGKAVETKDT------AKE-----AKE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
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                                                                                                                                                              DB 2; Length 448;
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                                                                                                                                                          7.8%; Score 175; DB 2; L 24.5%; Pred. No. 0.025;
Live 50; Mismatches 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5,
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Pred. No. 0.0042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 EKTPEEPKEEVTIKANLIYADGKTQTAEFKG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.78;
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A,Molecule type: protein
A,Residues: 1-74 <AKE>
C,Keywords: immunoglobulin
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Best Local Similarity
...thes 39; Conserva
                                                                                                                                                                                 Best Local Similarity
Matches 114; Conserv
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EALKNDD 72
                                                                                        A; Gene: At2g36640
A; Map position: 2
                                                                                                                  A; Map position:
                                                                                                                                                                 Query Match
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                                       late embryogenesis abundant protein-like - Arabidopsis thaliana
N;Alternate names: protein F8J2.210
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T47561
R;Nyakatura, G:; Fartmann, B:; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 DNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEAT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                230 EEPKEEV-TIKANLIYADGKTQ-----TAEFKGTFAEATAEAYRYADLLAKENGKYTADL 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 EDGGYTINIRFAGKKVDEKPEEPMDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYAND 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      346 ------MRLEGKKLDEDASR-------KTQQSTES--AADKAHETKDSVAQ 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAY----ADTLKK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 AEAYRYA-DALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 QTAEFKGTFEEATAE----AYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344 NGVDGEWTYDDATKTFTVTEKPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.1%; Score 182; DB 2; Length 47 ilarity 24.1%; Pred. No. 0.012; Conservative 59; Mismatches 195; Indels
                                                                                                                                                                                                               A; Reference number: 224458
A; Accession: T47561
A; Accession: T47561
A; Accession: T47561
A; Accession: T47961
A; Molecule type: DNA
A; Residues: 1-479 < NYA>
A; Crossreferences: EMBL: AL132969
A; Crossreferences: EMBL: AL132969
C; Genetics: Columbia; BAC clone F8J2
C; Genetics: Columbia; BAC clone F8J2
                                                                                                                                                                          Mayer, K.F.X. submitted to the Protein Sequence Database, April 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----ETAEKAFKQYANDNGVDGVWTYDDATK 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   439 RPGYVATVLKEADQMTGQTFNDVG----EIDDEEK 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 110; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 3
A;Introns: 329/3; 382/2
A;Note: F8J2.210
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RESULT 9
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Query Match Best Local Similarity 24.4%; Pred. No. 0.29; Matches 119; Conservative 57; Mismatches 172; Indels 140; Gaps 23; Qy 3 ENKETPETPETPETPETSEEVTIKANLIFANGSTOTA	OY 225 KEKTPEEPKEEVIKANLIYADGKTOTAEFKGTFAEATAEAYRYADLLAKENGKY 279 1 1 1 1 1 1 1 1 1 1	378 TTYKLVINGKTLKGETTTRAVDAETAEKAFKQYANDNGVDGVWTYDDA	RESULT 14 C95008 immunoglobulin Al proteinase [imported] - Streptococcus pneumoniae (strain TIGR4) C;Species: Streptococcus pneumoniae C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001 C;Accession: C95008 R;Tettelin, H: Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; H on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzappl nson, T. Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001 A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A;Reference number: A95000; MUID:21357209; PMID:11463916	
Justice and the control of the contr	Ouery Match Dest Local Similarity 24.2%; Pred. No. 0.059; Best Local Similarity 24.2%; Pred. No. 0.059; Matches 113; Conservative 50; Mismatches 161; Indels 142; Gaps 20; QY 3 ENKEETPETPETPETBEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYANDTLKKDNGE 62 Db 79 EARESTKGGAQIASEKAVGAKDATVEKAKETADYTAEKVGE 119 QY 63 YTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYANGGKTQTAEFKGTFEEATAEAY 122 Db 120 YKDYTUNKAKEKEKTPARKAKETANTARA VERNETAEKTETEY	123 RYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEGVIIKANLIYADGKTQTAEF 1 1 1 1 1 1 1 1 1 1	QY 231 EPREEVTIKANLIYADGKTQTAEFKGTFABATABAYRYADLLAKENGKYTADLED 285 DD 259 KLGELKDSAVETAKRAMGFLSGKTEEAKGKAVETKDTAKE	RESULT 13 T52485 To the control of

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C; Species: Streptococcus pneumoniae
C; Species: Streptococcus pneumoniae
C; Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
C; Accession: B98047
R; Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; F. F.; Hoskins, J.A.; Alborn Jr., W.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; DeHoff, B.S.; F. F.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A; Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A; Reference number: A97872; MUID:21429245; PMID:11544234
A; Accession: B98047
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: The Matsus DNA
A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                             672 GTDG---YKD-DYTFTVAKSKAEQPGVY--TSFKQLVTAMQSNLSGVYTLASDMTADEVS 725
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NIPYTTEEIQDPTLLKNRRKIERQG --- QAGTRTIQYEDYIVNGNVVETKEVSRTEVAPV 486
                                                                                                                                                                                                                                143 GYTLNIKFAGKEK-----TPEEPKEEVTIKANLI----YADGKTQTAEFKGTFEEA 189
                                                                                                                                                                                                                                                                                                                                                                190 TAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEEP-KEEV------TI 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 IRFAGKKVDEKPEEPMDTYKLILNGKT-----LKGETTTEAVDAATAEKVFKQYANDN 344
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23.0%; Pred. No. 1.5;
tive 46; Mismatches 162; Indels 150;
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Matches 107; Conservative
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Search completed: October 29, 2002, 09:31:33 Job time: 24.2057 secs

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Sequence S Sequence Sequence Sequence Sequence

Sequence 2, Ay Sequence 12, Sequence 38, Sequence 38, Sequence 10, Sequence 11, A Sequence 1, A Sequence 6, A

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1 AVENKEETPETPETDSEEEVIIKANLIFANGSTQTAEFKGTFEKATSEAYADTLKKDN 60
                                                                                                                                                                                                                                                                                                                       APPLICANT: Bjvrck, Lars
APPLICANT: Sjvbring, Ulf
TILLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/795,475 FILING DATE: 11-FEB-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 2235; DB 2;
100.0%; Pred. No. 1.8e-170;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
       US-09-117-233-16
US-09-117-233-18
US-09-117-233-18
US-09-058-459-38
US-09-117-233-18
US-09-117-233-18
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US-09-117-233-18
US-09-117-233-6
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US-09-058-459-43
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US-09-058-459-58
US-09-058-459-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: MCMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 100084.402D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 99104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08795475 Patent No. 5965390 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 434 amino acids
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
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STRANDEDNESS: un)
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Best Local Simi
Matches 434;
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                                                                            ; Search time 13.5074 Seconds
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Sequence
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1 AVENKEETPETPETDSEEEV......GVDGVWTYDDATKTFTVTEM
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
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         GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                       - protein search, using sw model
                                                                            October 29, 2002, 09:28:27
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Match Length D
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Length 434;

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MOLECULE TYPE: protein
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 JS-08-795-475-1
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                                                                                                                                                                                                                                                                                                                                                     1 AVENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDN
                              61 GEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAE
                                                                                          AYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Bjvrck, Lars
APPLICANT: Sjvbring, Ulf
TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli LE392/pHDL, DSM 7054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 100084.402D1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,475
FILING DATE: 11-FEB-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08795475 Patent No. 5965390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305 amino acids
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                 TYDDATKTFTVTEM 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                  181 EFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                    241 NLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKVD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                       61 GEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAE 120
                                                                                                         1 AVENKEETPETPETPETBEEEVIIKANLIFANGSTQTAEFKGTFEKATSEAXAYADTLKKDN 60
                                                                                     1 AVENKEETPETPETDSEEEVTIKANLIFANGSTOTAEFKGTFEKATSEAYAYADTLKKDN 60
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Patent No. 6162903
GENERAL INFORMATION:
APPLICANT: Trowerr, Angus R.
APPLICANT: Atkinson, Anthony
APPLICANT: Aurphy, Jonathan P.
APPLICANT: Laurence, Oliver S.
APPLICANT: Laurence, Oliver S.
TITLE OF INVENTION: IMMUNGGLOBULIN BINDING PROTEINS DERIVED
TITLE OF INVENTION: PROM L PROTEIN AND THEIR USES
NUMBER OF SEQUENCES: 12
Length 305;
                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OFFIGHT OF SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/446,137B FILING DATA: CLASSIFICATION FOR PAY 1995
                    2.6e-117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
  DB
                                            Mismatches
  Score 1565;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 100084.406
TELECOMMUNICATION INFORMATION:
           100.08; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: Floppy disk COMPUTER: IBM PC compatible ODERATING SYSTEM: PC-nocassopywapp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: McMasters, David D. REGISTRATION NUMBER: 33,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1027 amino acids
  70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seattle
Washington
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Query Match
Best Local Similarity
Matches 305; Conserv
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60 KGLTLNIKFAGKKEKPEEPKEEVTIKVNLIFADGKTQTAEFKGTFEEATAKAYAYADLLA 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 KGYILNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAYRYADALK 129
                                                                                                                                                                                                                                                                                                                                                                                                                          130 KDNGEYTVDVADKGYTLNIKFAGKE--KTPEEPKEEVTIKANLIYADGKTQTAEFKGTFE 187
                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                   10 ETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVAD
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APPLICANT: LINDBERG, Martin
APPLICANT: MUELLER, Hans-Peter
APPLICANT: RANTAMAKI, Liisa K.
TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING
TITLE OF INVENTION: PLASMAPROTEINASE INHIBITOR-BINDING PROTEINS
                                                                                                                                                                                                                                 ;
9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 DGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/669,408B
                                                                                                                                                                                            DB 4;
                                                                                                                                                                                                              . 6e-89
                                                                                                                                                                                                                               20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Washington STATE: D.C.
                                                                                                                                                                                          Score 1216;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE94/00826
FILING DATE: 06-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9302855-3
FILING DATE: 06-SEP-1993
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 2000/-JLC
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
~~wenther: IBM PC compatible
~~wenther: IBM PC Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
   (206) 622-4900
                                                                                                                                                                                            54.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JUL-1996
                   TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acids
                                                                           291 amino acids
                                                                                                                                                                                                                             Matches 241; Conservative
                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LA
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                                                                                                 TYPE: amino acid
                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                    US-08-446-137B-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               573
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                                                                                                                                                                                        EYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA 121
                                                                             Gaps
                                                                                                                61
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                                                                                                                                                                                                                                                                                                                                                                                                                                              634 HAGEETPELKDGYATYEEAEAAAKEALKNDDVNNAYEIVQGADGRYYY--VLKIEVADEE
                                         Length 1027;
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APPLICANT: Laurence, Oliver S.
APPLICANT: Laurence, Oliver S.
APPLICANT: Duggleby, Clive J.
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEINS DERIVED
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                   56.5%; Score 1263.5; DB 4; Length
58.8%; Pred. No. 1.5e-92;
.ive 36; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTIBLE
OPERATINE: PSYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
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NAME: MCMASters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 100084.406
TELECOMMUNICATION INFORMATION:
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FILING DATE: 22-MAY-1995
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Patent No. 6162903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Trowern, Angus R. APPLICANT: Atkinson, Anthony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                           Conservative
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MEDIUM TYPE: Floppy
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STATE: Washington
                                     Query Match
Best Local Similarity
Matches 281; Conserv
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US-08-446-137B-2
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TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
TITLE OF INVENTION: USING
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 DLAKKKKAADPQ-----SADTKSKLVK----LVVMVCEGLRFNTV----SRTV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DV---ADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQT-AEFKGTFAEATAEA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       266 YRYADLLAKENGKYTADLEDGGYTINIRFAGKKVDEKPE------EPMDTYKLILNGK 317
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                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 DAGFNSOHGVTLTVT-OGK----QVQKWDRISKAAFEWADHPTAVIPDMQKLGIKDKNEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           364 ---KPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVW
                                                                                                                                                                                                                                                                                                                                                                                                      83;
                                                                                                                                                                                                                                                                                                                                                                Length 502;
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PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                ; Score 622.5; DB 1;
; Pred. No. 6.3e-42;
36; Mismatches 136;
        . , ve
26-Jan-1995
N: 435
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Patent No. 5646026
Patent No. 5646026 5646119
                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFRENCE/DOCKET NUMBER: 3827:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: ANDREA T. BORUCKI
9330 ZIONSVILLE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
                                                                                                                                                                                                                                                                                                                                                                Query Match 27.9%;
Best Local Similarity 41.1%;
Matches 178; Conservative 30
                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 502 amino acids
TYPE: amino acid
                  CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
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CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                          linear
                                                        FILING DATE: 26 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                              US-08-378-761A-25
                                                                                                                                                                                                                                                                                        TOPOLOGY:
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Patent NO. 5635384
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICEE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
                                                                                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                                                                                                                                                              148 ANEIVNNSDAYTAESIQPLYKLINDAY---DVLESKDYSKY--DSQDKVNNLADQLRDAV 202
                                                                                                                                                                                                                                                                                                                                                                                                    80 ------GKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA--YRYA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 DALKKDNGEYTVDVADKGYTLNIKFA---GKEKTPEEPKEEVTIKANLIYADGKTQTAEF 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 KGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFA---GKEKTPEEPKEEVTIK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               371 GNTF--SGETTTRAIDAATAEKEFKQYATANGV---DGEWSYDDATKTFTVTEKPA---V 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300 DEKPE--EPMDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATK 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   417
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                                                                                                                                                                                                                                                                                                                            24 ANLIFANGSTQTAEFKGTFEKATSEAYAYADTLK-KDNGEYTVDVADKGYTL--NIKFA-
                                                                                                                                                                                                                                                                                                                                                                                                                                          203 QAVQLEAPTVIDAPELTPALTTYKLVVKGNTF -- SGETTTK -- -- AIDTATAEKEFKQYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 ANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358 TFTVTEKPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVD
                                                                                                                                                                                                                                                                                      51;
                                                                                                                                                                                                                                                    Length 664;
                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                              Query Match 31.6%; Score 706.5; DB 3; Best Local Similarity 43.9%; Pred. No. 1.9e-48; Matches 192; Conservative 51; Mismatches 143;
61743/102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PC-DOS/MS-DOS
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9330 ZIONSVILLE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Rioppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
              TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                    TELERAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
REFERENCE/DOCKET NUMBER:
                                                                                                                                : 664 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     418 GVWTYDDATKTFTVTEM 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         543 GVWTYDDATKTFTVTEM 559
                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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CITY: INDIANAPOLIS
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US-08-378-761A-25
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                                                                                                                                LENGTH:
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RIBOSOME-INACTIVATING PROTEINS, INACTIVE
PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
USING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---LLAKENGKYTADLEDGGYTINIRFAGKKVDEKPE-----EPMDTYKLILNGKTL 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KGETTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATKTFTVTE---------363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       364 -KPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVWTY 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKPEVIDASELTPAVTTYKLVINGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWTY 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEV---TIKANLIYADG---- 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82;
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                                                                                                                                                                                                                                                                                                                                                            COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,761A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---KTQTAEFKG------TFAEATAEAYRYAD-
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46.9%; Pred. No. 6.7e-42;
tive 28; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JAN-1995
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; Patent No. 5646026
; Patent No. 5646026 5646119
                                                                                                                                                                   ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (317) 337-4846 INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WALSH, TERENCE A
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MORGAN, ALICE ER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 3365
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LENGTH: 493 amino acids
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Best Local Similarity 46.9%
Matches 146; Conservative
TITLE OF INVENTION: RIBOTITLE OF INVENTION: PRECITIES OF INVENTION: USIN NUMBER OF SEQUENCES: 81 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-378-761A-23
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APPLICANT: WALSH, TAPPLICANT: HEY, TINAPPLICANT: MORGAN,
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                                                                                                                                                                                                                                                                                                                                    46268
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                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                   STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GVWWEFGKDGDTHLLGDNPRWLGFGGRYQD-LIGNKGLETVTMGRAEMTRAVN 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 DAGFNSQHGVTLTVT-QGK----QVQKWDRISKAAFEWADHPTAVIPDMQKLGIKDKNEA 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266 YRYADLLAKENGKYTADLEDGGYTINIRFAGKKVDEKPE------EPMDTYKLILNGK 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---KPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVW 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DV---ADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQT-AEFKGTFAEATAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37 EFKGTF-----EKATSEAYAYADTLKKDNGEYTVDV-ADKGYTLNIKFAGKEKTPEEPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 DHKGIFQPVLPPEKKVPELWFYTE-LKTRTSSITLAIRMDNLYLVGFRTPG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 DLAKKKKAADPQ-----SDTKSKLVK----LVVMVCEGLRFNTV----SRTV
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                                                                                                                       COMPUTER: IN TOPY WISH
COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN Release #1.0, Version #1.25
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.9%; Score 622.5; DB 1
41.1%; Pred. No. 6.3e-42;
                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/378761
FILING DATE: 26-JAN.1995
ATTORNEY/AGENT INFORMATION:
NAME: BORDCKI, ANDREA T
REGISTRATION NUMBER: 3351
REFERENCE/DOCKET NUMBER: 38272B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 23, Application US/08378761A Patent No. 5635384 GENERAL INFORMATION:

A APPLICANT: WALSH, TERENCE A APPLICANT: HEY, TIMOTHY D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (317) 337-4846 INFORMATION FOR SEQ ID NO: 25:
                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   502 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                COMPUTER READABLE FORM:
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                                                                                            MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                     FILING DATE:
                                  46268
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US-08-378-761A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-485-286-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 SEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLN 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
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APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Tarlinton, David M.
APPLICANT: Tarlinton, David M.
APPLICANT: Tarlinton, David M.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
                   APPLICANT: Treutlein, Herbert R.

TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
STORIET: 400 Garden City Plaza
CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15; Indels
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                                                                                                                                                                                                                                                 ZIP: 11530

CMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,741B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 618; DB 3;
Pred. No. 8.4e-42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Mismatches
                                                                                                                                                                                                                              United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/09160567 Patent No. 6326179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 1059
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 6;
APPLICANT: Tarlinton, David M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGIO. Frank S.
REGISTRATION NUMBER: 31,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.78;
75.98;
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LENGTH: 342 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 126; Conserv
                                                                                                                                                                                                             New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                     CITY: Gar
STATE: Ne
COUNTRY:
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RIBOSOME-INACTIVATING PROTEINS, INACTIVE PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF USING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 TVSRTVDAGFNSQHGVTLTVTQGKQVQKWDRISKAAFEWADHPTAVIPDMQKLGIKDKNE 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                271 ---LLAKENGKYTADLEDGGYTINIRFAGKKVDEKPE------EPMDTYKLILNGKTL 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 AARIVALVKNOTTAAAATAG-SVNV-----DKPEVIDASELTPAVTTYKLVINGKTL 283
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                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Datem: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 27.8%; Score 622; DB 1;
Best Local Similarity 46.9%; Pred. No. 6.7e-42;
Matches 146; Conservative 28; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/378761
FILING DATE: 26-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 38272B TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-828-741B-6
Sequence 6, Application US/08828741B
Patent No. 6043069
GENERAL INFORMATION:
APPLICANT: Koengen, Frank
APPLICANT: Suess, Gabriele M.
                                                            NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (317) 337-4846 INFORMATION FOR SEQ ID NO: 23:
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TITLE OF INVENTION:
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                                                                                                                                                                                                                              ZIP: 46268
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United States of America

ZIP: 11530

COUNTRY:

CITY: Garden City STATE: New York

STREET:

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RIBOSOME-INACTIVATING PROTEINS, INACTIVE
PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
USING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88 -----GVWWEFGKDGDTHLLGDNPRWLGFGGRYQD-LIGNKGLETVTMGRAEMTRAVN 139
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                                                                                                                                                                                                                                                                                                                                                                   37 EFKGTF-----EKATSEAYAYADTLKKDNGEYTVDV-ADKGYTLNIKFAGKEKTPEEPK 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150 FAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAYRYADLLAKENGKYTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 DAGFNSQHGVTLTVT-QGK----QVQKWDRISKAAFEWADHPTAVIPDMQKLGIKDKNEA
                                                                                                                                                                                                                                                                                                                                                                                            38 DHKGIFQPVLPPEKKVPELWFYTE-LKTRTSSITLAIRMDNLYLVGFRTPG-----
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                                                                                                                                                                                                                                                                                     27.7%; Score 618; DB 1; Length 489; 40.8%; Pred. No. 1.4e-41;
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                                                                                                                                                                                                                                                                                                                             35; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19, Application US/08485286
                   NAME: BORUCKI, ANDREA T
REGISTRATION UNUBER: 33651
REFERENCE/DOCKET NUMBER: 3827
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEO ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: ANDREA T. BORUCKI
9330 ZIONSVILLE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: HORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-TITLE OF INVENTION: PRECURSOR
TITLE OF INVENTION: USING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                489 amino acids
                                                                                                                                                                                                                                                                                                          Best Local Similarity 40.83
Matches 175; Conservative
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Patent No. 5646026 5646119
                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-378-761A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INDIANAPOLIS
                                                                                                                                                                                     amino acid
                                                                                                                                                                                                           linear
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                                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                                                                LENGTH:
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                                                                                                                                                                                                                                                                                         Query Match
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APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: USING
TITLE OF INVENTION: USING
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDREA T. BORUCKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ï
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 342;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EATAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,567
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Developatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 8.4e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 27.7%; Score 618; Best Local Similarity 75.9%; Pred. No. 8 Matches 126; Conservative 5; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,761A
FILING DATE: 26-JAN-1995
                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: DiG19110, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4346
TELEPRIS: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19, Application US/08378761A Patent No. 5635384 GENERAL INFORMATION:
                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,741
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: ANDREA T. BORUCKI
9330 ZIONSVILLE ROAD
                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                               342 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INDIANAPOLIS
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                                                                                                                                                              CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-160-567-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116
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PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Diciglio, Frank S.
REISTRATION NIMBER: 31,346
REFERENCE/POCKET NUMBER: 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (516) 742-436
TELERX: (516) 742-436
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
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                                                                        Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                               New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-828-741B-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----GVWWEFGKDGDTHLLGDNPRWLGFGGRYQD-LIGNKGLETVTMGRAEMTRAVN 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         150 FAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAYRYADLLAKENGKYTV 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    282 ETTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATKTFTVTEKPEVIDASELTPAVTRSK 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 EFKGTF-----EKATSEAYAYADTLKKDNGEYTVDV-ADKGYTLNIKFAGKEKTPEEPK 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210 DV----ADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQT-AEFKGTFAEATAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     234 ARIVALVKNQT-----TAAAATAGSKPEVIDASELTPAVTTYKLVINGKTLKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    365 PEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVWTYDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 DHKGIFQPVLPPEKKVPELWFYTE-LKTRTSSITLAIRMDNLYLVGFRTPG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13, Application US/08828741B
Patent No. 6043069
GENERAL INFORMATION:
APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Traulinton, David M.
AITLE OF INVENTION: CATALITIC ANTIBODIES AND A METHOD OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 175; Conservative 35; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATKTFTVTE-----
                         SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.7%; Score 618; DB 1; 40.8%; Pred. No. 1.4e-41;
                                                                                                         PILLING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/378761
FILING DATE: 26-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERRENCE/DOCKET NUMBER: 38272B
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                          APPLICATION NUMBER: US/08/485,286
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                        489 amino acids
                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-485-286-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            402 ATKTFTVTE 410
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US-08-828-741B-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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78 FAGKEKTPEE---------PKEEVTIKANLIYADGKTQTAEFKGTFEEA 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 EEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLNIK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 27.5%; Score 615; DB 3; Length 178; Best Local Similarity 76.2%; Pred. No. 5.9e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13, Application US/09160567
Patent No. 6326179
GENERAL INFORMATION:
APPLICANT: Suess, Gabriele M.
APPLICANT: Tariliton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 TAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPK 161
                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,741B
FILING DATE: 26-MAR-1997
E: SCULLY, SCOTT, MURPHY & PRESSER 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 Garden City Plaza CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
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                                                                                                      United States of America
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/160,567

FILING DATE:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/828,741

FILING DATE:

APPLICATION NUMBER: 08/828,741

FILING DATE:

APPLICATION NUMBER: 01,346

REGISTRATION NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 31,346

REFERENCE/OCKET NUMBER: 31,346

REFERENCE/SOCKET NUMBER: 31,346

REFERENCE (516) 742-343

TELEPHONE: (516) 742-343

TELEPHONE:
```

Search completed: October 29, 2002, 09:31:57 Job time : 16.5074 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

October 29, 2002, 09:25:06; search time 34.0622 Seconds (without alignments) 1415.233 Million cell updates/sec Run on:

US-08-325-278B-3
2235
1 AVENKEETPETPETDSEEEV......GVDGVWTYDDATKTFTVTEM 434 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

747574 seqs, 111073796 residues Searched:

747574 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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15. (SIDSI/gcddata/geneseqy-embl/AA1991.DAT:*
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17. (SIDSI/gcddata/geneseqy-embl/AA1991.DAT:*
18. (SIDSI/gcddata/geneseqy-embl/AA1991.DAT:*
19. (SIDSI/gcddata/geneseqy-embl/AA1991.DAT:*
21. (SIDSI/gcddata/geneseqy-embl/AA1991.DAT:*
22. (SIDSI/gcddata/geneseqy-embl/AA1991.DAT:*
22. (SIDSI/gcddata/geneseqy-embl/AA2001.DAT:* A_Geneseq_032802:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

!			Description	Sequence encoding		Amino acid sequenc						Streptococcus Prot	,	Sequence of polype
			ID	AAR42994	AAR42993	AAB31372	AAB10432	AAR42203	AAR43699	AAR42204	AAR71929	AAR62944	AAR10005	AAP70468
			DB	14	14	22	21	14	14	14	16	15	12	œ
			Match Length DB	434	305	467	367	1027	1027	291	664	593	594	480
	æ	Query	Match	100.0	70.0	69.4	61.4	56.5	56.5	54.4	31.6	31.4	31.4	31.0
			Score	2235	1565	1550	1372	1263.5	1263.5	1216	706.5	702	701.5	692.5
		Result	No.	-	2	3	4		9	7	80	6	10	11

Protein G variant Protein G. Strept Protein G. Strept Protein G variant Streptococcus GX78 Streptococcus Prot	H 4	Protein G variant. Protein G variant. Protein G variant. Type 3 GX7809 prot IgG-binding Strept Protein G variant.	Protein G variant. Type 9 GX7809 prot IgG-binding Strept Protein G variant. Protein G variant. Type 2 GX7809 prot IgG-binding Strept	Type 8 GX7809 prot [1965-binding Strept Protein G variant. Protein G variant. Type 1 GX7809 prot 196-binding Strept Protein G variant.
AAR07014 AAP70493 AAP95030 AAR07013 AAR10004	AAR53295 AAR10011 AAR53294 AAY57610 AAP94785	AAR07004 AAP94784 AAR07003 AAR10009 AAR53293 AAP94787	AAR07011 AAR10015 AAR53299 AAR94783 AAR0002 AAR10007	AAR10013 AAR53298 AAR07001 AAR10008 AAR53291 AAR07010 AAR94788 AAR07006
11 10 11 12 15	15 12 15 21 21	12211	112 112 113 113 113 113 113 113 113 113	12 12 13 14 15 10 10 10
5 4 4 4 4 4 4 8 8 4 4 4 8 8 4 4 8 8 8 8	269 265 265 185 235	22 11 14 14 16 16 16 16 16 16 16 16 16 16 16 16 16	1100 1100 1100 1100 100	201 201 148 148 148 201 201 269 269
	30.2 30.2 30.2 30.0 29.8		00000000	9999999999
692 683 683 683 683	675 674 674 670	003330 00330 0003 0003	0003 0003 0003 0003 0003 0003 0003 000	6663 6683 6683 6688 6686 6686 6686 6686
122 133 14 17	18 20 21 22	2 2 2 2 2 2 3 4 3 4 3 4 3 4 3 4 3 4 3 4	1 21 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	W W W W W A A A A A A A A A A A A A A A

ALIGNMENTS

AAR42994 standard; Protein; 434 AA. (6-MAY-1994)(first entry) AAR42994

Sequence encoding immunoglobulin light chain binding protein.

Immunoglobulin; light chain; binding; identification; purification; separation; ss.

E. coli L392/pHDLG, DSM 7055.

/label= B1 immunoglobulin light chain binding 81..305 /label= B2 immunoglobulin light chain binding /label= B3 immunoglobulin light chain binding Location/Qualifiers 5..305 domain. domain. domain. 153..305 225..305 Domain Oomain от в шос

/label= B4 immunoglobulin light chain binding /label= B5 immunoglobulin light chain binding domain. domain. 297..305 Оощаin Jomain Jomain

/label= C1 immunoglobulin heavy chain binding 309..434

Domain

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us-08-325-278b-3.rag

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421 TYDDATKTFTVTEM 434
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                                                                        /label= C2 immunoglobulin heavy chain binding
364..434
/label= D intermediate immunoglobulin heavy
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Matches 434; Conservative
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The protein (Protein L) is capable of binding to immunoglobulin G light chains. It is useful for binding, separating (purifying) and identifying immunoglobulin and for removing immunoglobulin molecules from serum. Hybrid proteins of the L protein can bind all human immunoglobulin classes and many immunoglobulins from other species. They are highly soluble and retain their binding activity at high without loss over a pH range of 3-10. They can be immobilised without loss of activity.
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                                                                                                                                                                                                                     Immunoglobulin; light chain; binding; identification; purification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New protein L binding light chains of all immunoglobulin classes - for binding purifying and identifying immunoglobulin, also related DNA, vectors and host cells
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/label= Bl immunoglobulin light chain binding
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Pred. No. 1.4e-84;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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AAR42993 standard; Protein; 305
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Best Local Similarity 100.0%; Pi
Matches 305; Conservative 0;
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N-PSDB; AAQ50452.
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N-PSDB; AAA71428
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                                                                                     120
                                           121 AYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTA 180
                                                                                                                   EFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKA 240
                                                                                                                                                              NLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKVD 300
                                                                                                                                                                                                                                                                                                                                                                       production; food processing; protein antibiotic; feed enzyme; L: CBD cex protein; cell signal peptide.
           09
                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of protein L/CBD cex/ER retaining peptide fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Expressing and isolating recombinant protein in a plant, useful fo producing large quantities of recombinant proteins, by expressing fusion protein including a cellulose binding peptide fused to a
GEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CBDT-) CBD TECHNOLOGIES LTD.
(YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
                                                                                                                                                                                                                                                                                   AAB31372 standard; Protein; 467 AA.
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EKPEE 305
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manufacturing leather or alcoholic beverages, pectinesterases for pectin hydrolysis in food industry, lipses for cleaving ester linkage in triglycerides, and for effluent treatment. The recombinant proteins may further be used to produce protein antibiotics, which can be used in healing processes, and to produce animal feed enzymes. The present sequence represents a fusion protein of the invention, and comprises a fusion of a cell signal peptide, protein L, CBD cex, and an endoplasmic reticulum retaining peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 AYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTA 180
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                                                                                                                                                                                                                                                                                                 Length 467;
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                                                                                                                                                                                                                                                                                                                                                         43;
                                                                                                                                                                                                                                                                                                    DB 22;
                                                                                                                                                                                                                                                                                              Score 1550; DB 22
Pred. No. 1.8e-83;
3; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Moldenhauer G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB10432 standard; Protein; 367
                                                                                                                                                                                                                                                                                                    69.48;
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                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-499832/45.
                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 328; Conserv
                                                                                                                                                                                                                                               467 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Breitling F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JAN-1999;
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281;
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Peptide
                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                    antibodies (MAb) which comprises (i) fusing B lymphocytes with myeloma cells to produce antibody-producing hybridomas such that the antibodies cells to produce antibody-producing hybridomas by an antibody-binding protein (I); and (ii) binding the antibody to antigens (Ag). The combination of the signal peptide of a murine immunoglobulin (Ig) Kappa chain or a murine MHC (major histocompatibility complex) Class I k(k) molecule; an antibody-binding site of proteins A, G, L or LG, and the transmembrane domain of PDERFK (platelet-derived growth factor receptor) or CDS2. The method is used to select MAb with specificity for particular antigens. MAb can be selected without separate culture of hybridomas, and selection can be made against many antigens in a library, optionally on the basis of strength of affinity for a particular antigen. Complex mixtures of hybridomas can be used for selection, reducing the time and cost involved in MAb selection. This sequence represents the protein G, Neo-R and the bla protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                              ÷,
                                                                                           This invention describes a novel method for the selection of monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 VDVADKGYTLNIKFACKEKTPEEPKEEVIIKANLIYADGKTQTAEFKGTFEEATAEAYRY 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAYRY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADCKTQTAEFKG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 TFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIY 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKVDEKPE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 KEKTPEEP----KEEVIKANLIYADGKTQTAEFKGTFEEATAEAYRYADALKKDNGEYT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                        5 KEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYT 64
           Selecting monoclonal antibodies, by expressing them on the surface only bybridomas attached to antibody-binding protein, then reaction with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide; immunoglobulin; binding; analysis; purification; ELISA;
                                                                                                                                                                                                                                                                                                                                                                                   Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                61.4%; Score 1372; DB 21;
82.4%; Pred. No. 3.6e-73;
ive 19; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 EPMDTYKLILNGKTLKGETTTEAVDAATA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             321 SEED ---- LNG-AVDGQNDTSQTSSPSA 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enzyme linked immunoabsorbant assay
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                                                                Claim 16; Fig 1; 22pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 82.4 ses 271; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptococcus magnus
                                                                                                                                                                                                                                                                                                                                                        367 AA;
                                      antibody library
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                                                                                                                                                                                                                                                                                                                                                        Sequence
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----ET-----TTEAVDAATAEKVFKQYAND-----NGVDGEWTYDDATKTFTVTEK 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The synthetic immunoglobulin binding proteins derived from protein L correspond to the repeated sequences inprotein L which bind immunoglobulin kappa light chains. They can be used in protein analysis, purification procedures and other blochemical processes e. ELISA. The synthetic molecules are of particular advantage if they are free of regions in protein L which exhibit albumin and cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVWTY 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPGEDTPEVQEGYATYE-----EAEAAKEALKEDKVNNAYEVVQGADGRYYY 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YRYADALKKDNGEYTVDVADKGYTLNIKFAGKE---KTPEEPKEEVTIKANLIYADGKTOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           514 IKVNLIFADGKTQTAEFKGTFEEATAEAYRYADLLAKVNGEYTADLEDGGYTINIKFAGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKE---KTPEEPKEEVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238 IKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  K-----VDE-----KPEEPM-----DTY-KLILNGKTLKG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 14; Length 1027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New immunoglobulin binding proteins derived from Protein {\tt L} -which bind immunoglobulin kappa light chains but not albumin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                     Trowern AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Signal sequence.
60..968
/label= Mature protein L.
                                                                                                                                                                                                                                                                                                                                                    (PUBL-) PUBLIC HEALTH LAB SERVICE BOARD
                                                                                                                                                                                                                                                                                                                                                                                                  Murphy JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Figure 1; 28pp; English.
                                                                                                                                                                                                                     93WO-GB00950
                                                                                                                                                                                                                                                                    92GB-0009804
92GB-0026928
                                                                                                                                                                                                                                                                                                                                                                                                     CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  Atkinson A, Duggleby
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         wall binding.
                                                                                                                                                                                                                   07-MAY-1993;
                                                                                                                                                                                                                                                                       07-MAY-1992;
                                                                                                          W09322439-A
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K-----KPEEPM-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291 AA;
                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAQ50947
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                                                                                                                                                     18-MAY-1994
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                                                                                                                                                                                                                                                                                                                    Atkinson A,
                                                                                                                                                                                                                             WO9322439-A.
                                                                                                                                                                                                                                             11-NOV-1993
                                                                                                                                                                                                              Synthetic.
                                                                                                                                      AAR42204;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YRYADALKKDNGEYTVDVADKGYTLNIKFAGKE--KTPEEPKEEVTIKANLIYADGKTQT 179
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKE--KTPEEPKEEVT
                                                                                                                                                                                                                                                                                                                                          Protein L forms a complex with immunoglobulin Kappa light chain. Purified protein can be used as a reagent for immobilising antibodies e.g. on columns, in diagnostic tests and in assays. may also be used in the production of pharmaceuticals.
                                                                                                                                                                                                                                                                                                                                                                                                  DB 14; Length 1027
                                                                                                                                                                                                                                                                                             used for prodn.
                                                                              Protein; immunoglobulin; binding; immobilisation; light chains;
                                                                                                                                                                                                                                                                                                                                                                                                                  90; Indels
                                                                                                                                                                                                                                                                                          Immunoglobulin binding polypeptide, protein L - used for of pharmaceuticals and for immobilising antibodies e.g. columns, in diagnostic tests and in assays
                                                                                                                                                                                                                                                     Trowern AR;
                                                                                                                                                                                                                                                                                                                                                                                                  56.5%; Score 1263.5; DB 58.8%; Pred. No. 2.7e-66; ive 36; Mismatches 90
                                                                                       antibodies; diagnosis; pharmaceutical; ss
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                                                                                                                             36..59
/label= Signal sequence.
60..968
/label= Mature protein I
                                                                                                                                                                                                                                   (PUBL-) PUBLIC HEALTH LAB SERVICE BOARD.
                                                                                                                                                                                                                                                     Murphy JP,
                ¥Ÿ.
                                                                                                                     Location/Qualifiers
               AAR43699 standard; Protein; 1027
                                                                                                                                                                                                                                                                                                                          Claim 4; Figure 1; 29pp; English.
                                                                                                                                                                                                     93WO-GB00949
                                                                                                                                                                                                                    92GB-0009804
                                              (first entry)
                                                                                                                                                                                                                                                    Duggleby CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                   WPI; 1993-368797/46.
P-PSDB; AAR43699.
                                                                                                                                                                                                                                                                                                                                                                                  1027 AA;
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Les 281; Conserv
                                                                                                       magnus
                                                                                                                                                                                                     07-MAY-1993;
                                                                                                                                                                                                                    07-MAY-1992;
                                                                                                      Peptococcus
                                              18-MAY-1994
                                                                                                                                                                    WO9322438-A.
                                                                                                                                                                                                                                                    Atkinson A,
                                                                                                                                                                                     11-NOV-1993
                                                               Protein L.
                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                               AAR43699;
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                             Peptide
                                                                                                                                             Protein
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           574 EQPGENPGITIDEWLLKNAKEEAIKELKEAGITSDLYFSLINKAKTVEGVEALKNEILKA 633
                                                                                                                  -TIEAVDAATAEKVFKQYAND-----NGVDGEWTYDDATKTFTVTEK 364
.-- 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The synthetic immunoglobulin binding proteins derived from protein L comprise repeated sequences from protein L which bind immunoglobulin kappa light chains. They can be used in protein analysis, purification procedures and other biochemical processes e. g. ELISA. The synthetic molecules are of particular advantage if they are free of regions in protein L which exhibit albumin and cell wall binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVAD 69
                                                                                                                                                                                                                                     365 PEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVWTY 422
                                                                                                                                                                                                                                                                          EPGEDTPEVQEGYATYE------EAEAAAKEALKEDKVNNAYEVVQGADGRYYY 739
                                                                                                                                                        Peptide; immunoglobulin; binding; analysis; purification; ELISA; enzyme linked immunoabsorbant assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New immunoglobulin binding proteins derived from Protein L - which bind immunoglobulin kappa light chains but not albumin or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
-----DTY-KLILNGKTLKG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunoglobulin binding protein derived from protein L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trowern AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54.4%; Score 1216; DB 14;
82.5%; Pred. No. 3.9e-64;
iive 20; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PUBL-) PUBLIC HEALTH LAB SERVICE BOARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murphy JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR42204 standard; Protein; 291 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 12; Figure 2; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93WO-GB00950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92GB-0009804
92GB-0026928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 241; Conservative
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17;

us-08-325-278b-3.rag

δ <u>8</u> g ò g

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AAR71929 RESULT

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obtain prods. for sepn., detection or quantification or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= al
/note= "linking region"
179..215
/label= A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA.
                              English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           593
                                                                                                                                   31.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR62944 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106..140
/label= A1
141..178
                              50pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                  Query Match
Best Local Similarity 43.99
Matches 192; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVWTYDDATKTFTVTEM 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus sp. GX7805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               543 GVWTYDDATKTFTVTEM
                              Disclosure; Page 31;
 to obtain prods. for binding inhibition
                                                                                                               664 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR62944;
                                                                                                               Sequence
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          EATAEAYRYADILLAKENGKYTVDVADKGYTLNIKFAGKE--KTPEEPKEEVTIKANLIYA 245
                                                   KDNGEYTVDVADKGYTLNIKFAGKE--KTPEEPKEEVTIKANLIYADGKTQTAEFKGTFE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding fast alpha 2-macro:globulin-binding proteins - used
                                                                                DGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rantamaki LK;
                                                                                           /note= "putative wall anchoring motif" 539..664
                                                                                                                                                                                                                                      fast alpha-2-macroglobulin binding protein; FAM; na proteinase-inhibitor binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "cell wall spanning region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "membrane spanning domain"
                                                                                                                                                                                                                                                                                                                               /label= IgG1
/note= "IgG binding domain 1"
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279.348
/label= IgG2
'~^te= "IgG binding domain 2'
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/1abel- IgG3
^ate= "IgG binding domain 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mueller H,
                                                                                                                                                                                                                                                                                                                                                                                                                            /label= IgG4
/note= "IgG binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= IgG5
/note= "IgG binding domain
                                                                                                                                                                                                                                                                      Streptococcus dysgalactiae strain SC1
                                                                                                                                                                                                                                                                                                     1..30
/label=_Sig_peptide
                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                        A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lindberg M,
                                                                                                                                                      AAR71929 standard; Protein; 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94WO-SE00826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93SE-0002855
                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                         .278
                                                                                                                                                                                                                                                                                                                                                                                                                                               .558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-123382/16.
N-PSDB; AAQ89196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JONSSON H.
LINDBERG M.
MUELLER H.
                                                                                                                                                                                                                    S. dysgalactiae MIG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-SEP-1993;
                                                                                                                                                                                               22-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09507296-A
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                                                                                                                                                                           AAR71929;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (COSS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (LIND/)
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                                                                                                                                                                                                                                                                                                    Peptide
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                                                                                                                                                                                                                                                  plasma
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130
                   120
                                       188
                                                           180
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analyzed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               257 TANNVD-GEWSYDDATKTFTVTEKPAVIDAPELTPALTTYKLIVKGNTF--SGETTT--- 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            482
                                                                                                                                                                                                                                                                                                                                                                                                 ------GKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA--YRYA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 DALKKDNGEYTVDVADKGYTLNIKFA---GKEKTPEEPKEEVTIKANLIYADGKTQTAEF 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 DEKPE--EPMDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATK 357
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 ANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 ANLIFANGSTQTAEFKGTFEKATSEAYAYADTLK-KDNGEYTVDVADKGYTL--NIKFA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 KGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFA---GKEKTPEEPKEEVTIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51;
                                                                                                                                                                                                                                         Length 664;
A phage lambda GEM-11 library of S. dysgalactiae SCl DNA was a for fast-acting alpha-2-macroglobulin (FAM)- and IgG-binding activity. One clone, which expressed both activities, was analyzed to obtain DNA encoding the FAM-binding protein, MIG (AAR71929). The mig gene is given in AA089196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus Protein G; variant; IgG binding activity; immunoglobulin; Lancefield Group G; bacterial Fc receptor
                                                                                                                                                                                                                                   ; Score 706.5; DB 16; Length
; Pred. No. 7.4e-34;
51; Mismatches 143; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus Protein G derived from strain GX7805.
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17;

Region

Domain

Region

Region

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160 LSDFLKSQTP-----AEDTVKSIELAEAKVLANRELDKYQVSDYHKNLINNAKTVEGVK 213
                                                                                                                                                                                                               207 YTVDVADKGYTLNIK-FAGKEKTPEE-----PKEEVTIKANLIYADGKTQTAEFKGTFAE 260
                                                                  -----KTQTAEFKGTFEEATAEAYRYADALKKDNGE---YTVDVADKGYTLNIKFAGKEK 155
                                                                                                                                                                                                                                                                   A--TAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKVDEKPE------EPMDTY 310
                                                   45 ATSEAYAYADTLKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYA-DG 103
                             Gaps
                                                                                                                                                                               KLILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATKTFTVTEKPEVIDA
                                                                                                                                                            156 TPEEPKEEVTIKANLIYA-DG----KTQTAEFKGTFEEATAEAYRYAD---LLAKENGK
                           60;
  Length 593;
                           Indels
                        28; Mismatches 132;
31.4%; Score 702; DB 15; 48.1%; Pred. No. 1.2e-33;
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444..498
/label= Active Site B2
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/label= Active Site
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86US-0854887.
87WO-US00329.
87US-0063959.
88US-0209236.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
Query Match 31.4%
Best Local Similarity 48.1%
Matches 204; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        374..428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus sp GX7805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulins; Ig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENE-) GENEX CORP.
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495 VTEM 498
                                                                                                                                                                                                                                                                                                                                                                                                                             431 VTEM 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-MAY-1989;
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17-FEB-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Active-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-DEC-1990
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20-JUN-1988
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                                                                                                                                                                                                                                                                   261
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                                                                                                                                                                                                                                                                                                                       311
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    useful for

                                                                                                    /label= B1
/note= "involved in 1gG binding activity"
358..372
                                                                                                                                                                                                                                                                                                      'note= "involved in IgG binding activity"
                                                                                                                                          /label b
/note "linking region"
373..427
/label B3
/note "involved in IgG binding activity"
376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant streptococcal protein G variants - antibody detection and purification and for therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "corresponds to GAA codon"
                                                                                                                                                                                                                         'note= "corresponds to CCT codon"
                                                                            /note= "corresponds to GGA codon"
                                                                                                                                                                                                                                                                                                                                  codon"
                                                                                                                                                                                                                                                                                                                                /note= "corresponds to ACT
           /label= a2
/note= "linking region"
254..290
                                                                                                                                                                                                                                                               /note= "linking region"
443..497
/label= B2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                860S-0829354.
860S-0854887.
870S-0063959.
880S-0209236.
900S-0540169.
                                                                                                                                                                                                                                                                                                                                              /label= Cl
536..540
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/label= C2
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/label- C3
                                                                                                                                                                                                                                                                                                                                                                                                                          546..550
/label= C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                   551..555
/label= C5
                                                 label= A3
                                                                                                                                                                                                                                      428..442
/label= b
                                                                                        .357
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N-PSDB; AAQ75036.
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                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                  Misc-difference
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                                                                                                                                                                                                            Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pahnestock SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-FEB-1986;
23-APR-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-FEB-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-APR-1992;
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                                                                                                                                                                       Active-site
                                                                                                                                                                                                                                                                             Active-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            are claimed
                                                                                         Active-site
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Region

Region Region

Region

Region

370

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KTPEEPKE-----EVTIKANLIYA-DG----KTQTAEFKGTFEEATAEAYRYADALKK 130
                                                                                                                                                                                                                                                   A recombinant DNA molecule containing a nucleotide sequence which codes for a protein or polypeptide having the same igG specificity protein G from Streptococcus G148 (AAN70757) is claimed. See, for example, AAN70754, AAN70755 and AAN70756.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 DNGE---YTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYA-DG-----KTQTAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 ANRELDKYGVSDYHKNLINNAKTVEGVKDLQAQVVESAKKARISEATDGLSDFLKSQTP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 KTVEGVKDLQAQVVESAKKARISEATDGLSDFLKSQTP----AEDTVKSIELAEAKVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 FKGTFEEATAEAYRYAD---LLAKENGKYTVDVADKGYTLNIK-FAGKEKTPEE----P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----AEDTVKSIELAEAKVLANRELDKYGVSDYYKNLINNAKTVEGVKALIDEILAALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEEVTIKANLIYADGKTQTAEFKGTFAEA - - TAEAYRYADLLAKENGKYTADLEDGGYTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNGVDGEWTYDDATKTFTVTEKPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAET
                                                                                                                                                                            New recombinant DNA molecules - for producing proteins with IgG-binding specificity of protein G or proteins A and G
                                                                                                                                                                                                                                                                                                                                                         Score 692.5; DB 8
                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEKAFKQYANDNGVDGVWTYDDATKTFTVTEM 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sites
                                                                                                    Uhlen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 303..372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus sp. Lancefield Group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ΑA
                                                                                                    Flock JI,
                                                                                                                                                                                                                                                                                                                                                   31.0%; Scor
49.7%; Pred
ative 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                593
                                                                                                                                                                                                                         Example; Fig 2; 39pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein G variant with three
87WO-SE00145
                             86SE-0001325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                       Matches 195; Conservative
                                                                                                    BM, Lindberg KM,
                                                          (PHAA ) PHARMACIA AB
                                                                                                                                 WPI; 1987-277686/39
                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR07014 standard;
                                                                                                                                                                                                                                                                                                                            480 AA
                                                                        (GUSS/) GUSS B M.
                                                                                                                                                 N-PSDB; AAN70757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunoglobulin.
20-MAR-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JAN-1991
                             21-MAR-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Active-site
                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR07014;
                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          403
                                                                                                                                                                                                                                                                                                                                                                                                                    83
                                                                                                       Guss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                           Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΩY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  οp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         435
                                                                                                                                                                                                                                                                                                              45 ATSEAYAYADTLKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYA-DG 103
                                                                                                                                                                                                                                                                                                                                 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                              267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      430
                                                                                                                                                             Protein G gene product may be modified allowing the variant to
be imobilised and exhibit different binding profiles. The bound
protein is useful in purification and detection of Igs and fragments.
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 ----KTQTAEFKGTFEEATAEAYRYADALKKDNGE---YTVDVADKGYTLNIKFAGKEK
                                                                                                                                                                                                                                                                                                                                                                                                    160 LSDFLKSQTP-----AEDTVKSIELAEAKVLANRELDKYGVSDYHKNLINNAKTVEGVK
                                                                                                                                                                                                                                                                                                                                                                                                                                156 TPEEPKEEVTIKANLIYA-DG-----KTQTAEFKGTFEEATAEAYRYAD---LLAKENGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                    YTVDVADKGYTLNIK-FAGKEKTPEE----PKEEVTIKANLIYADGKTQTAEFKGTFAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---EPMDTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVWTYDDATKTFT
                                                                                                                                                                                                                                                                                 59;
                                                                                      Immobilised protein G variants - used for detection, isolation and purificn. immunoglobulin(s) and immunoglobulin fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of
                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261 A--TAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKVDEKPE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activity
                                                                                                                                                                                                                                                   31.4%; Score 701.5; DB 12; ilarity 47.9%; Pred. No. 1.3e-33; Conservative 28; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence of polypeptide possessing IgG-binding protein G from Streptococcus G148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibody-binding; IgG; IgA; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP70468 standard; Protein; 480 AA.
               Ψ
                                                                                                                                Disclosure; Fig 9; 52pp; English
               Wroble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
             Lee T,
                                           WPI; 1991-006758/01
                                                                                                                                                                                                                                                                 Local Similarity
les 203; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus G148
                                                                                                                                                                                                                         594 AA;
                                                          O-PSDB; Q10002
               Fahnestoc SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |||||
VTEM 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VTEM 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAY-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-SEP-1987
                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                     Query Match
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376

268 207

436 431 496

RESULT

17;

Gaps

65;

Indels

107; .; 8

Length 480;

186

181 131 342

402 353

as

Best Loca Matches

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protein G expressed by inserting the gene into an expression vector. A second vector may also be used as a cryptic helper plasmid to stably maintain the first plasmid in the host cell. Bacterial Fc receptors such as Protein G can be used to detect and purify antibodies, and in the treatment of disease. Fc receptors are useful to purify antibodies to be used in the purifien. of protein drugs and as therapeutics. High levels of Protein G can be obtd. in conditions favourable for isolation, using a non-pathogenic host. Suitable cloning vectors are lambda gtll, M13mp9 and pGX1066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 KDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYAD-GKTQTAEFKGTFEE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93 AAWEAAAAADALAKAKADALKEFNKYGVSDYYKNLINNAKTVEGIKDLQAQVVESAKKAR 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45 RNGGELT------NLLGNSETTLALRNEESATADLTAAAVADTVAAAAAENAGA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 ATAEAYRYADLLA-----KENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIYA-DG-----KTQTAEFKGTFAEATAEAYRYAD---LLAKENGKYTADLEDGGYTINI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cloned Protein G gene – used for producing Protein G for detection and purificn. of antibodies and treatment of diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.6%; Score 683; DB 8; Length 448; 53.2%; Pred, No. 1.1e-32; tive 15; Mismatches 92; Indels
                                                                                                                                                                                                                       Streptococcus Lancefield Group G strain.
                                                                                                                                                                                                                                                                           /label=active site B1
298..352
/label=active site B2
                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                  AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig. 3; 68pp; English.
                                                                                                                                                                                           Protein G; antibody; Fc receptor;
                                                                                AAP70493 standard; protein; 448
                                                                                                                                                                                                                                                                                                                                                                                         87WO-US00329
                                                                                                                                                                                                                                                                                                                                                                                                                    86US-0854997
86US-0829354
                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1987-250197/35.
N-PSDB; AAN70811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
hes 176; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FAHN/) FAHNESTOCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENE-) GENEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   448 AA;
             495 VTEM 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ahnestock S;
                                                                                                                                                                                                                                                                                                                                                                                          17-FEB-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                     22-APR-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                  14-FEB-1986;
                                                                                                                                                                                                                                                                                                                                     WO8705025-A
                                                                                                                                                                                                                                                                 Active-site
                                                                                                                                                                                                                                                                                           Active-site
                                                                                                                                                                                                                                                                                                                                                                27-AUG-1987
                                                                                                                                      06-MAR-1991
                                                                                                                                                                 Protein G.
                                                                                                            AAP70493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
                                                      RESULT 13
                                                                     AAP70493
                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261 A--TAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKVDEKPE------EPMDTY 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45 ATSEAYAYADTLKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYA-DG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVWTYDDATKTFT 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              311 KLILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATKTFTVTEKPEVIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----KTQTAEFKGTFEEATAEAYRYADALKKDNGE---YTVDVADKGYTLNIKFAGKEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 LSDFLKSQTP----AEDTVKSIELAEAKVLANRELDKYGVSDYHKNLINNAKTVEGVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPEEPKEEVTIKANLIYA-DG-----KTQTAEFKGTFEEATAEAYRYAD---LLAKENGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 DLQAQVVESAKKARISEATDGLSDFLKSQTP-----AEDTVKSIELAEAKVLANRELDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YTVDVADKGYTLNIK-FAGKEKTPEE----PKEEVTIKANLIYADGKTQTAEFKGTFAE
                                                                                                                                                                                                                                                                                                                                                                                                                                Fragments and variants of the sequence are claimed esp. where incorporated into a non-pathogenic host eg. E.coli, and expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The variants have a higher binding efficiency and capacity for immunoglobulin, and may be used for purifying, detecting and isolating antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 11; Length 593;
                                                                                                                                                                                                                                                                                                                                                               encoding Protein G from Streptococcus sp., used for binding
                                                                                                                                                                                                                                                                                                                                                  Recombinant Protein G variants - obtd. using a cloned gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.0%; Score 692; DB 11; Length 594 47.9%; Pred. No. 4.6e-33; Live 28; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 9; 48pp; English.
                                                                                                                                                             88US-0209236.
86US-0829354.
86US-0854887.
87WO-US00329.
87US-0063959.
                                                                                                                                    88US-0209236
             373..427
/label=B3
443..497
/label=B2
/label=B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 47.9 Matches 203; Conservative
                                                                                                                                                                                                                                                                                                      WPI; 1990-297491/39.
N-PSDB; AAQ06019.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                593 AA;
                                                                                                                                                                                                                                                                                                                                                                             immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              high levels.
                                                                                                                                                                                                                                                                            Fahnestock SR;
                                                                                                                                                                                                                                                  GENE-) GENEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          431 VTEM 434
                                                                                                                                    20-JUN-1988;
                                                                                                                                                                                                                       19-JUN-1987;
              Active-site
                                       Active-site
                                                                               US4956296-A
                                                                                                          11-SEP-1990
                                                                                                                                                                              14-FEB-1986
                                                                                                                                                                                          23-APR-1986
17-FEB-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             268
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203 INNAKTVEGVKELIDEILAALPKTDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYAND 262
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                                           expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant Protein G variants - obtd. using a cloned gene encoding Protein G from Streptococcus sp., used for binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fragments and variants of the sequence are claimed esp. incorporated into a non-pathogenic host eg. E.coli, and at high levels.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.6%; Score 683; DB 11;
53.2%; Pred. No. 1.1e-32;
iive 15; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                      Streptococcus sp. Lancefield Group G strain.
                                                                                      EKAFKQYANDNGVDGVWTYDDATKTFTVTEM 434
                                                                                                     Protein G variant with two active sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 8a-c; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                            A
                                                                                                                                                                                        AAR07013 standard; protein; 448
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86US-0854887.
87WO-US00329.
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298..352
/label=B2
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es 176; Conserv
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23-APR-1986;
17-FEB-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          293 RFAGKKVDEKPE------EPMDTYKLILNGKTLKGETTTEAVDAATAEKVFKQXAND 343
               --EPMDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYAND 343
                                                                       NGVDGEWTYDDATKTFTVTEKPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETA 403
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203 INNAKTVEGVKELIDEILAALPKTDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYAND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expressing proteins having immunoglobulin-binding properties protein G and derived from Streptococcus sp.
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Best Local Similarity 53.2%; Pred. No. 1.1e-32;
Matches 176; Conservative 15; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                      ds.
                                                                                                                                              EKAFKQYANDNGVDGVWTYDDATKTFTVTEM 434
                                                                                                                                                                                                                                                                                                                                                     Fc receptor;
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N-PSDB; AAN91093.
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             293 RFAGKKVDEKPE-
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	Oy 242 LIYA-DG	QQ	93	A AWEAAAAADALAKAKADALKEFNKYGVSDYYKNLINNAKTVEGIKDLQAQVVESAKKAR	152
	Db 153 ISBATDGLSDFLKSQTPAEDTVKSIELAEAKULANRELDKYGVSDYHKNL 202 Qy 293 RFAGKKVDEKPEEPMDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYAND 343	Οy	242	LIYA-DGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINI	292
	Oy 293 RFAGKKUDEKPEEPMDTYKLILNGKTLKGETTTEAVDAATAEKVEKOYAND 343 Db 203 INNAKTVEGVKELIDEILAALPKTDTYKLILNGKTLKGETTTEAVDAATAEKVEKOYAND 262 Qy 344 NGVDGEWTYDDATKTETVTEKPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETA 403 Db 263 NGVDGEWTYDDATKTETVTEKPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETA 322 Qy 404 EKAFKQYANDNGVDGVWTYDDATKTETVTEM 434	qq	153	SEATOGLSDFLKSQTPSDYHKNL	202
	Db 203 INNAKTECVKELIDEILAALPKTDTYKLILNGKTIKGETTTEAVDAATAEKKQYAND 262 Qy 344 NGVDGEWTYDDATKTTYTERPEVIDASELTPAVTTYKLVINGKTLKGETTTRAVDAETA 403 [11111111111111111111111111111111111	ΟŊ	293	RFAGKKVDEKPEEPMDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYAND	343
344 263 404 323	OY 344 NGVDGEWTYDDATKTFTVTEKPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETA 403	qq	203	INNAKTVEGVKELIDEILAALPKTDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYAND	262
263 404 323	Db 263 NGVDGEWTYDDATKTFTVTEKPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETA 322 Qy 404 EKAFKQYANDNGVDGVWTYDDATKTFTVTEM 434	οy	344	NGVDGEWTYDDATKTFTVTEKPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETA	403
	Oy 404 EKAFKOYANDNGVDGVWTYDDATKTFTVTEM 434	QQ	263	NGVDGEWTYDDATKTFTVTEKPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETA	322
323	Db 323 EKAFKQYANDNGVDGVWTYDDATKTFTVTEM 353 Search completed: October 29, 2002, 09:29:29	Qy	404	EKAFKQYANDNGVDGVWTYDDATKTFTVTEM 434	
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Scoring table:

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017464 caenorhabdi
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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MEDLINE-93094283; PubMed-1460053;
Kihlberg B.M., Sjobring U., Kastern W., Bjorck L.;
"Protein LG: a hybrid molecule with unique immunoglobulin binding
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Last annotation update)
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EMBL: S50809; AAA03280.1; -.
HSSP; P06654; 1PGX.
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InterPro; IPR0003147; B1.
InterPro; IPR000724; IgG_bind_B.
Pfam; PF02246; B1; 4.
Pfam; PF01378; IgG_binding_B; 2.
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NCBI_TaxID=1306;
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2556.865 Million cell updates/sec
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                                                                                                                                                                            1 AVENKEETPETPETDSEEEV.......GVDGVWTYDDATKTFTVTEM 434
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           GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                 562222 seqs, 172994929 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                          October 29, 2002, 09:25:41
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Score

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murphy J.P., Trowern A.R., Duggleby C.J., "Nucleotide sequence of the gene for peptostreptococcal protein L.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNG 61
FKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKAN
                                                                                                                                                                                   KPEEPMD-TYK = - LILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVD-GEWTYDDATK
                                                                                                                                                                                               358 TFTVT------EKPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETAE
                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptostreptococcus magnus.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.5%; Score 1263.5; DB 2;
58.8%; Pred. No. 1.8e-53;
tive 36; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                       992 AA
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Pfam; PF00746; Gram_pos_anchor; 1.
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MEDLINE=95078460; PubMed=7987012;
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EMBL: L04466; AAA67503.1; -.
HSSP; Q51911; 1GAB.
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Best Local Similarity 58.8
Matches 281; Conservative
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InterPro; IPR002988; GA.
InterPro; IPR001899; Gra
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25
992 AA;
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                                                                                                                                                                                                       VTEKPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVW 420
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Kastern W., Holst E., Nielsen E., Sjobring U., Bjorck L.;
"Protein L, a bacterial immunoglobulin-binding protein and possible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNG
                                                        181 EFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKA
                                                                                                                                                                     Peptostreptococcus magnus.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
Finegoldia.
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BJDLINE-9216971; PubMed-1618782;

BJOERCK L., Sjoebbing U., Kastern W.;

Structure of peptostreptococcal protein L and identification of repeated immunoglobulin light chain-binding domain.";

EMDL, Repeated immunoglobulin light chain-binding domain.";

EMDL, Rohen. 267:12820-12825(1992).

EMDL, M86697; AAA256121.

EnterPro; IPR001899; Gram_pos_anchor.

Fran; PF02246: B1; S.

Pfam; PF00746; Gram_pos_anchor: 1.
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Infect. Immun. 58:1217-1222(1990)
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719 PR(
78983 MW;
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Q53291 streptococc Q51912 peptostrept Q51918 peptostrept Q53975 streptococc Q91f88 arabidopsis Q32646 arabidopsis Q96246 arabidopsis Q91255 petromyzon Q94k2 lactobacill Q9wza6 thermotoga Q9u266 plasmodium Q53837 salmonella Q9u8g8 manduca sex Q9jyk4 neisseria m
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ALIGNMENTS

Q53291 Q53291; 01-NOV-1996 (TEMBLrel. 01, Cr 01-NOV-1996 (TEMBLrel. 01, Lr 01-NOV-2001 (TEMBLrel. 19, Lr

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InterPro; IPR000724; IgG_bind_B.
Pfam; PF02246; B1; 4.
Pfam; PF01378; IgG_binding_B; 2.
NON_TER 455 455
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MEDLINE=93094283; PubMed=1460053;
Kihlberg B.M., Sjobring U., Kastern W., Bjo
"Protein LG: a hybrid molecule with unique
                                                                                                                                                                                                                                        EMBL; S50809; AAA03280.1;
HSSP; P06654; 1PGX.
                                                                                                                                                                                                                                                      properties.";
J. Biol. Chem. 267:25583-25588(1992).
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                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus sp.
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        82
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                                                  GEYTYDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAE 120
GEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAE
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05; Conservative
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Pred. No. 9.1e-79;
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"Structure of peptostreptococcal protein L and identification repeated immunoglobulin 11ght chain-binding domain.";
J. Biol. Chem. 267:12820-12825(1992).
EMBL, M86697; AAA25612.1; ...
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InterPro: IPR001899; Gram_pos_anchor.
Pfam; PF02246; B1; 5.
Pfam; PF00746; Gram_pos_anchor; 1.
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Bacteria; Firmicutes; Bacillus/Clostridium
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        182
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                                                 215
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                                                                                                                                                                                                                              VENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNG
                                                                                                                                                                                                        VENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNG
FKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKAN
                                                                                                                       EYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA
                                                                                                                                            EYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA
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llarity 100.0%;
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719 P
78983 MW;
                                                                                                                                                                                                                                                                                         Score 1561; DB 2; ; Pred. No. 2.5e-78; 0; Mismatches 0;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
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protein
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Best Local :
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SIGNAL
CHAIN
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01-NOV-1996
01-DEC-2001
                                                                                                                                                                                                            SEQUENCE
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EMBL; L04466; AAA67503.1; -.
HSSP; Q51911; IGAB.
                                                                                                                                                                                                                                                                                                                                                                                                               Q51918;
Q51918;
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InterPro; IPR002988; GA.
InterPro; IPR001899; Gra
                                                                                                                                                                                                                                         Pfam;
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 539
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                                                       ---EQPGE 543
              KVDEKPEE 305
                           IKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGK
                                                                                     EYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA
                                                                                                                                                MERKLSEKETPE--PEEEVTIKANLIFADGSTQNAEFKGTFAKAVSDAYAYADALKKDNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246;
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                                                                                                                                                                                                                                                                                                                                      FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                  PRECURSOR.
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25
992 AA;
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992 PR'
108700 MW;
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79.98;
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10,
                                                                                                                                                                                                                                                                                                                 Duggleby C.J.;
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                                                                                                                                                                            Score 1226.5; DB 2;
Pred. No. 8.5e-60;
2; Mismatches 31;
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                                                                                                                                                                                                          POTENTIAL.
PROTEIN L.
W; 9CFF5771578A5DCE CRC64;
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